

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 17:33:36 / Search time 171 Seconds
(without alignments)
1637.512 Million cell updates/sec

Title: US-10-760-407-2

Perfect score: 3737
Sequence: 1 MSARTPLPTLNEDTDEPT.....SGTSMAFKRIASKINELKT 724

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq.16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3737	100.0	724	ABU08527	Abu08527 Human ser
2	3737	100.0	724	ABR43964	Abx43964 Human ser
3	3737	100.0	724	AD130081	Adi30081 Human kin
4	3737	100.0	724	ADQ60236	Adq60236 Human kin
5	3736	100.0	724	AAE19051	Aae19051 Human PAR
6	3700.5	99.0	777	ABR43968	Abx43968 Human ser
7	3699	99.0	780	ABR43967	Abx43967 Human ser
8	3670.5	98.2	787	AD196619	Ad196619 Human ser
9	3654	97.8	722	ABR43965	Abx43965 Rat serin
10	3654	97.8	722	AD130083	Adi30083 Rat serin
11	3654	97.8	722	ADQ60238	Adq60238 Rat serin
12	3644	97.5	722	AAE88227	Aae88227 Rat neuro
13	3640	96.6	796	ABU1830	Abu1830 Human MDD
14	3589.5	96.1	799	AD140876	Adi40876 Human kin
15	3566	95.4	691	AAE19050	Aae19050 Human PAR
16	3566	95.4	691	ABR43966	Abx43966 Human ser
17	3555	95.1	804	AAW79333	Aaw79333 Human pro
18	3550.5	95.0	768	AAW78349	Aaw78349 Human pro
19	3515	94.1	745	AAE33550	Aae33550 Human mtc
20	3515	94.1	745	ABR43970	Abx43970 Serine/ch
21	3515	94.1	745	ADC34768	Adc34768 Human ser
22	3515	94.1	745	ADG91722	Adg91722 Human mtc
23	3515	94.1	745	ADL14100	Adl14100 Human ser
24	3515	94.1	745	ADQ15058	Adq15058 Human can
25	3467	92.8	774	ABR43969	Abx43969 Serine/ch

26	3425	91.7	731	7	ADC99074	Adc99074 Human KPP
27	2555	68.4	793	5	ADC34764	Adc34764 Rat serin
28	2552	68.3	795	5	AAE19052	Aae19052 Human PAR
29	2552	68.3	795	5	AAE16258	Aae16258 Human kin
30	2552	68.3	795	8	ADQ88278	Adq88278 Human 138
31	2546	68.1	795	6	AAE33551	Aae33551 Human mtc
32	2546	68.1	795	7	ADG91723	Adg91723 Human mtc
33	2453	65.6	779	2	AAE98226	Aae98226 Rat neuro
34	2419.5	64.7	744	5	AAE19049	Aae19049 Human PAR
35	2414	64.6	737	8	AD140874	Adi40874 Human kin
36	2399.5	64.2	729	2	ABG73795	Abg73795 Murine MA
37	2399	64.2	729	4	AAW37158	Aaw37158 Human Twe
38	2399	64.2	729	4	AAE65628	Aae65628 Novel pro
39	2389	64.2	729	6	AAE33552	Aae33552 Human mtc
40	2389	64.2	729	7	ADC34765	Adc34765 Human C-T
41	2389	64.2	729	7	ADG91724	Adg91724 Human mtc
42	2399	64.2	729	8	AD129234	Adi29234 Human MAR
43	2399	64.2	729	8	AD129438	Adi29438 Human MAR
44	2395.5	64.1	776	7	ADE40427	Ade40427 Human MAR
45	2388	63.9	713	6	ABU07562	Abu07562 Human ser

ALIGNMENTS

RESULT 1
ID ABU08527 standard; protein; 724 AA.
XX ABU08527;
AC
XX
DT 30-MAY-2003 (first entry)
XX
DE Human serine/threonine protein kinase.
XX
KW Human; enzyme; serine/threonine protein kinase; chromosome 11;
KM gene therapy.
XX
OS Homo sapiens.
XX
PN US6492156-B1.
XX
PD 10-DEC-2002.
XX
PF 31-OCT-2001; 2001US-00984890.
XX
PR 31-OCT-2001; 2001US-00984890.
XX
PA (PEKE) PE CORP NY.
XX
PI Yan C, Li Z, Neelam B, Difrancesco V, Beasley EM;
XX
DR WPI; 2003-327315/31.
XX
N-PSDB; ABX93647, ABX93648.
XX
PT Novel nucleic acid molecule encoding a kinase polypeptide related to
PT serine/threonine kinase subfamily; useful in development of human
PT therapeutics and diagnostic compositions.
XX
PS Claim 1; Fig 2; 107pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule consisting of
CC comprising of a cDNA sequence or genomic sequence (appearing as ABX93647
CC and ABX93648) encoding a kinase polypeptide that is related to the
CC serine/threonine kinase subfamily, or their complements. Also included
CC are a nucleic acid vector comprising the nucleic acids and a host cell
CC containing the vector and used to produce the protein. The nucleic acids
CC are useful in treatment and for identifying a compound that can be used
CC to treat a disorder associated with nucleic acid expression of the kinase
CC gene, as query sequences to perform a search against sequence databases
CC (for e.g. identify other family members or related sequences), as primers
CC for PCR (to amplify any given region of a nucleic acid molecule), to
CC synthesise antisense molecules of desired length and sequences, for

CC constructing recombinant vectors, expressing antigenic portions of the
 CC proteins, as probes for determining the chromosomal positions of the
 CC nucleic acid molecules by in situ hybridisation, making vectors
 CC containing the gene regulatory regions of the nucleic acid molecules,
 CC designing ribozymes, constructing host cells expressing the nucleic
 CC acids, and constructing transgenic animals. The nucleic acids are also
 CC useful as hybridisation probes, and for drug screening to identify
 CC compounds that modulate kinase nucleic acid expression (and to monitor
 CC the effectiveness of the compounds). The gene for the kinase is located
 CC on chromosome 11. The present sequence represents the human kinase of the
 CC invention

XX
 SQ Sequence 724 AA:

Query Match 100.0%; Score 3737; DB 6; Length 724;
 Best Local Similarity 100.0%; Pred. No. 5,4e-253;
 Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MSSARTPLPTLNERDTEQPTLGHLDSPSSKSNMIRGNSATSADQPHIGNRLKKTIG 60
Db 1 MSSARTPLPTLNERDTEQPTLGHLDSPSSKSNMIRGNSATSADQPHIGNRLKKTIG 60
QY 61 KGNFAKVKLARHILITGKEVAVKIIDKTQUNSSSLQQLFREVRIMKVLNPNIVKLEFVIE 120
Db 61 KGNFAKVKLARHILITGKEVAVKIIDKTQUNSSSLQQLFREVRIMKVLNPNIVKLEFVIE 120
QY 121 TEKTLVLMVEYASGGEVFDYLVAHGMRKEKARAKRQVVSAYOYCHQKFIYHRDIKAEN 180
Db 121 TEKTLVLMVEYASGGEVFDYLVAHGMRKEKARAKRQVVSAYOYCHQKFIYHRDIKAEN 180
QY 181 LLLDADNMNIIADPGFSNEFTFGNKLDTEFCGSPPYAAPLFQKKYDGEVDVWSLGVTL 240
Db 181 LLLDADNMNIIADPGFSNEFTFGNKLDTEFCGSPPYAAPLFQKKYDGEVDVWSLGVTL 240
QY 241 YTLVSGSLPPDQGNLKELRERVLRGKYRIPFYMSDTCENLLKKFLLNDSKRGTLLEQIMK 300
Db 241 YTLVSGSLPPDQGNLKELRERVLRGKYRIPFYMSDTCENLLKKFLLNDSKRGTLLEQIMK 300
QY 301 DRMMNVGHEBDELKPYVEPLPDYKDPRTTELAMVSMGYRREIODSLVGRYENWATYTL 360
Db 301 DRMMNVGHEBDELKPYVEPLPDYKDPRTTELAMVSMGYRREIODSLVGRYENWATYTL 360
QY 361 LGYKSELESGDTITTLKPRPSADLTNSAPSPSHKVQSVSNAPKORRFSDQGAIPISN 420
Db 361 LGYKSELESGDTITTLKPRPSADLTNSAPSPSHKVQSVSNAPKORRFSDQGAIPISN 420
QY 421 SYSKKTQSNNAENKRPREDREGSKKASTAKYPASPLPGLERKKTTPPSTNVSJSTGN 480
Db 421 SYSKKTQSNNAENKRPREDREGSKKASTAKYPASPLPGLERKKTTPPSTNVSJSTGN 480
QY 481 RSRNSPLERASLGQASIONGKOSTAPORVPVAPSPSAHNISSSGAPDRTFNPPRGVSSRS 540
Db 481 RSRNSPLERASLGQASIONGKOSTAPORVPVAPSPSAHNISSSGAPDRTFNPPRGVSSRS 540
QY 541 TTHAGGLRQVROOQNPYGVTVPASPSGHSQGRGASGSIFSKFTSKFVRNINBESKOR 600
Db 541 TTHAGGLRQVROOQNPYGVTVPASPSGHSQGRGASGSIFSKFTSKFVRNINBESKOR 600
QY 601 VETLRPHVVGSGNDKEKEEFREAKPRSLRFTWSKTTSSMEPNMMEIRKVLIDANSCQ 660
Db 601 VETLRPHVVGSGNDKEKEEFREAKPRSLRFTWSKTTSSMEPNMMEIRKVLIDANSCQ 660
QY 661 SELHKRYMLLCHMGTPGHEDFVQWEMEYCKLPRLSLNGVRFKRIISGTSMAFNKIASKIAN 720
Db 661 SELHKRYMLLCHMGTPGHEDFVQWEMEYCKLPRLSLNGVRFKRIISGTSMAFNKIASKIAN 720
QY 721 ELKL 724
Db 721 ELKL 724

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RESULT 2
 ABR43964

ID ABR43964 standard; protein; 724 AA.
 XX ABR43964;
 AC
 XX
 DT 11-AUG-2003 (first entry)
 DE Human serine/threonine protein kinase 661_protcd.
 XX
 KW Serine/threonine protein kinase; cytosolic; antidiabetic; nootropic;
 KW neuroprotective; antiinflammatory; analgesic; gene therapy; human;
 KM chromosome 11q12-q13; enzyme.
 XX
 OS Homo sapiens.
 XX
 PN WO2003033708-A2.
 XX
 PD 24-APR-2003.
 XX
 PF 14-OCT-2002; 2002MO-EP011478.
 XX
 PR 15-OCT-2001; 2001US-0328804P.
 PR 27-FEB-2002; 2002US-0359688P.
 PR 01-JUL-2002; 2002US-0392365P.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Koehler RH;
 XX
 DR WPI; 2003-403226/38.
 DR N-PsDB; ACC48080.
 XX
 PT New polynucleotide encoding a serine/threonine protein kinase
 PT polypeptide, useful for preventing, ameliorating or treating diseases
 PT associated with the protein kinase dysfunction, e.g. cancer, diabetes or
 PS a CNS disorder.
 XX
 PS Claim 1; Page 138-141; 175dp; English.
 XX
 CC The invention relates to human serine/threonine protein kinase
 CC polypeptide and encoding polynucleotides. The polypeptides can be
 CC expressed by standard recombinant methodology. The polynucleotide and
 CC polypeptide are useful in preventing, ameliorating or treating diseases
 CC associated with serine/threonine protein kinase dysfunction. The diseases
 CC include cancer, diabetes, a CNS disorder or chronic obstructive pulmonary
 CC disease. These can also be used to treat pain associated with the above
 CC disorders. The protein kinase is also used in various diagnostic assays
 CC or in genetic testing. The present sequence represents a human serine/
 CC threonine protein kinase 661_protcd
 XX

SQ Sequence 724 AA:

Query Match 100.0%; Score 3737; DB 6; Length 724;
 Best Local Similarity 100.0%; Pred. No. 5,4e-253;
 Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MSSARTPLPTLNERDTEQPTLGHLDSPSSKSNMIRGNSATSADQPHIGNRLKKTIG 60
Db 1 MSSARTPLPTLNERDTEQPTLGHLDSPSSKSNMIRGNSATSADQPHIGNRLKKTIG 60
QY 61 KGNFAKVKLARHILITGKEVAVKIIDKTQUNSSSLQQLFREVRIMKVLNPNIVKLEFVIE 120
Db 61 KGNFAKVKLARHILITGKEVAVKIIDKTQUNSSSLQQLFREVRIMKVLNPNIVKLEFVIE 120
QY 121 TEKTLVLMVEYASGGEVFDYLVAHGMRKEKARAKRQVVSAYOYCHQKFIYHRDIKAEN 180
Db 121 TEKTLVLMVEYASGGEVFDYLVAHGMRKEKARAKRQVVSAYOYCHQKFIYHRDIKAEN 180
QY 181 LLLDADNMNIIADPGFSNEFTFGNKLDTEFCGSPPYAAPLFQKKYDGEVDVWSLGVTL 240
Db 181 LLLDADNMNIIADPGFSNEFTFGNKLDTEFCGSPPYAAPLFQKKYDGEVDVWSLGVTL 240
QY 241 YTLVSGSLPPDQGNLKELRERVLRGKYRIPFYMSDTCENLLKKFLLNDSKRGTLLEQIMK 300

```

Db	241	YTLVSGSLPFDGQNLKELRERVLRGKYRIPEYMSDTCENLTKKFLILNPSKRGTLQIMK	300	FT	Active-site	/note="Casein kinase II phosphorylation site"
Qy	301	DRMNVNGHEDDELKPYVEPLPDYKDPRTTLMVSMGYTRREIQLDSLVGQRYNEVMATYLL	360	FT	Modified-site	/note="Serine/threonine protein kinase active site"
Db	301	DRMNVNGHEDDELKPYVEPLPDYKDPRTTLMVSMGYTRREIQLDSLVGQRYNEVMATYLL	360	FT	Modified-site	/note="Serine/threonine protein kinase active site"
Qy	361	LGYSSELEGGTITLTKPRPSADLTNSSAPSPSHKVQSVSANPKQRRPSDAGPATPTSN	420	FT	Region	231..251
Db	361	LGYSSELEGGTITLTKPRPSADLTNSSAPSPSHKVQSVSANPKQRRPSDAGPATPTSN	420	FT	Modified-site	/note="Helix 1"
Qy	421	SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLGLERKKTTPPTNSVLSTSTN	480	FT	Modified-site	275..278
Db	421	SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLGLERKKTTPPTNSVLSTSTN	480	FT	Modified-site	/note="Casein kinase II phosphorylation site"
Qy	481	RSRNSPLLEBASLGQASIQNGKSTAPQRPVVASPSAHN1SSSGAPDRNPFRCVSSRS	540	FT	Modified-site	290..292
Db	481	RSRNSPLLEBASLGQASIQNGKSTAPQRPVVASPSAHN1SSSGAPDRNPFRCVSSRS	540	FT	Modified-site	/note="Protein kinase C phosphorylation site"
Qy	541	TFHAGQLRQVRDQONLPYGVTPASPSGSHSQRRASGSIPTSKFTSPKVRN1LNPSSKOR	600	FT	Modified-site	291..294
Db	541	TFHAGQLRQVRDQONLPYGVTPASPSGSHSQRRASGSIPTSKFTSPKVRN1LNPSSKOR	600	FT	Modified-site	/note="cAMP- and cGMP-dependent protein kinase phosphorylation site"
Qy	601	VELLRPHVVGSGGNDKEKEEFREAKPRSLRFTWSMKTSSMEPNEMMRIRKVLNDNSCQ	660	FT	Modified-site	338..341
Db	601	VELLRPHVVGSGGNDKEKEEFREAKPRSLRFTWSMKTSSMEPNEMMRIRKVLNDNSCQ	660	FT	Modified-site	/note="Casein kinase II phosphorylation site"
Qy	661	SELHEKXMLCMHGITRGHEDFVQWEMEVCKLPRLSLNGVFPKRIISGTSMAFKNIASKIAN	720	FT	Modified-site	348..353
Db	661	SELHEKXMLCMHGITRGHEDFVQWEMEVCKLPRLSLNGVFPKRIISGTSMAFKNIASKIAN	720	FT	Modified-site	/note="Casein kinase II phosphorylation site"
Qy	721	ELKL 724		FT	Modified-site	366..369
Db	721	ELKL 724		FT	Modified-site	/note="Casein kinase II phosphorylation site"
RESULT 3						
ID	AD130081	standard; protein; 724 AA.				
AC	AD130081;					
DT	22-APR-2004	(first entry)				
XX	Human kinase protein.					
XX	Human; kinase; serine/threonine kinase; immune response; drug screening;					
KW	tissue typing; pharmacogenomic analysis; tumour;					
KW	brain anaplastic oligodendroglioma; lung carcinoma tissue;					
KW	soft tissue leiomyosarcoma; gene therapy; transgenic animal; cytostatic;					
KW	enzyme.					
OS	Homo sapiens.					
XX						
XX						
FT	Key	Location/Qualifiers				
FT	Modified-site	3..5				
FT	Modified-site	/note="Protein kinase C phosphorylation site"				
FT	Modified-site	10..13				
FT	Modified-site	/note="Casein kinase II phosphorylation site"				
FT	Modified-site	29..31				
FT	Modified-site	/note="Protein kinase C phosphorylation site"				
FT	Modified-site	42..45				
FT	Modified-site	/note="Casein kinase II phosphorylation site"				
FT	Modified-site	59..62				
FT	Modified-site	/note="Protein kinase ATP-binding site"				
FT	Modified-site	75..78				
FT	Modified-site	/note="Casein kinase II phosphorylation site"				
FT	Modified-site	75..77				
FT	Modified-site	/note="Protein kinase C phosphorylation site"				
FT	Modified-site	90..93				
FT	Modified-site	/note="N-glycosylation site"				
FT	Modified-site	121..123				
FT	Modified-site	/note="Protein kinase C phosphorylation site"				
FT	Modified-site	133..136				

[illegible]

Db	361	LGYYSSLEEDPTITLKERPSADLTNAPSPPSHVQSVSANPKQRFESQAGALPTSN	420
Qy	421	SYSKTOSNNAENKRPEDEDSGRKASSTAKVPASPLPLGERKKTTPTPTNSVLTSTYN	480
Db	421	SYSKTOSNNAENKRPEDEDSGRKASSTAKVPASPLPLGERKKTTPTPTNSVLTSTYN	480
Qy	481	RSRNSPLLEBASIGQASIQNGKSTAPQRPVPVAPSAHNTSSGCGAPDRTNFPRGVSSRS	540
Db	481	RSRNSPLLEBASIGQASIQNGKSTAPQRPVPVAPSAHNTSSGCGAPDRTNFPRGVSSRS	540
Qy	541	TFHAGQLQVRDQONLPYGVTPASPESHSGRGCASGISIFSKTSTSPVRNLTNPPSKDR	600
Db	541	TFHAGQLQVRDQONLPYGVTPASPESHSGRGCASGISIFSKTSTSPVRNLTNPPSKDR	600
Qy	601	VELTRPHVVGSGNDYKKEEFREAKRSLRFTWSMKTSSMEBNEMREIRKVLDNSCO	660
Db	601	VELTRPHVVGSGNDYKKEEFREAKRSLRFTWSMKTSSMEBNEMREIRKVLDNSCO	660
Qy	661	SELHEKKMLLCMHGTGPHEDFVQMEWEVCKLPILSLNGRFRIRISGTSMAPFKVIASKIAN	720
Db	661	SELHEKKMLLCMHGTGPHEDFVQMEWEVCKLPILSLNGRFRIRISGTSMAPFKVIASKIAN	720
Qy	721	ELKL 724	
Db	721	ELKL 724	
RESULT 4			
ADQ60236	ID	ADQ60236 standard; protein, 724 AA.	
XX	AC	ADQ60236;	
XX	DT	07-OCT-2004 (first entry)	
XX	XX		
DE	XX	Human kinase.	
XX	XX		
KW	XX	allelic variant; orthologue; therapeutic; kinase activity modulation;	
KM	XX	kinase associated disorder; human; kinase;	
KW	XX	serine/threonine kinase subfamily; enzyme.	
XX	XX		
OS	XX	Homo sapiens.	
XX	XX		
FH	Key	Location/Qualifiers	
FT	Region	3..5	
FT	Region	/note= "protein kinase C phosphorylation site"	
FT	Region	10..113	
FT	Region	/note= "casein kinase II phosphorylation site"	
FT	Region	29..31	
FT	Region	/note= "protein kinase C phosphorylation site"	
FT	Region	42..45	
FT	Region	/note= "casein kinase II phosphorylation site"	
FT	Region	59..82	
FT	Region	/note= "protein kinase ATP-binding region signature"	
FT	Region	75..78	
FT	Region	/note= "casein kinase II phosphorylation site"	
FT	Region	75..77	
FT	Region	/note= "protein kinase C phosphorylation site"	
FT	Region	90..93	
FT	Region	/note= "N-glycosylation site"	
FT	Region	121..123	
FT	Region	/note= "protein kinase C phosphorylation site"	
FT	Region	133..136	
FT	Region	/note= "casein kinase II phosphorylation site"	
FT	Region	222..225	
FT	Region	/note= "Amidation site"	
FT	Region	275..278	
FT	Region	/note= "casein kinase II phosphorylation site"	
FT	Region	290..292	
FT	Region	/note= "protein kinase C phosphorylation site"	
FT	Region	291..294	
FT	Region	/note= "cAMP and cGMP dependent protein kinase	


```

Db      421 SYSKKTQSNNAENKPEEDRESGRKASSTAKVPASPLPELERKKTTPPTSTNSVLSTSTN 480
Qy      481 RSRNSPLLERASLIGASIONGKSDTAPORVPVSPASAHNISSSGGAPDRINPFRGVSRS 540
Db      481 RSRNSPLLERASLIGASIONGKSDTAPORVPVSPASAHNISSSGGAPDRINPFRGVSRS 540
Qy      541 TPHAQOLQVROOQNLPGVTPASPSPSGHSQGRGASGSIFFSKFTSKFYPRNLNEPESKDR 600
Db      541 TPHAQOLQVROOQNLPGVTPASPSPSGHSQGRGASGSIFFSKFTSKFYPRNLNEPESKDR 600
Qy      601 VETLRPHVVGSGGNKEKEEFREAKPRSLRFTWSMKTTSSMEPNMMEIRKVLDAWSCQ 660
Db      601 VETLRPHVVGSGGNKEKEEFREAKPRSLRFTWSMKTTSSMEPNMMEIRKVLDAWSCQ 660
Qy      661 SELHKRWMLCMHGTPGHEDFVQWMEVCKLPRLSLNGVRPKRISGTSMAFKNIASKIAN 720
Db      661 SELHKRWMLCMHGTPGHEDFVQWMEVCKLPRLSLNGVRPKRISGTSMAFKNIASKIAN 720
Qy      721 ELKL 724
Db      721 ELKL 724

```

RESULT 5

AAE19051 ID AAE19051 standard; protein; 724 AA.

AAE19051; AC

18-JUN-2002 (first entry)

Human PAR-1 β beta protein.

Human; Dishevelled associated kinase; PAR-1 kinase; enzyme; PAR-1 α ; PAR-1 β alpha; PAR-1 β beta; PAR-1 γ ; cancer; hyperproliferative disease; antisense therapy; Dsn.

Homo sapiens.

Location/Qualifiers

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FH      274 /note= "Encoded by AGG of the inverse complementary
FT      strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT      275 /note= "Encoded by TGC of the inverse complementary
FT      strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT      276 /note= "Encoded by CTG of the inverse complementary
FT      strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT      277 /note= "Encoded by ACA of the inverse complementary
FT      strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT      278 /note= "Encoded by CTT of the inverse complementary
FT      strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT      279 /note= "Encoded by TTG of the inverse complementary
FT      strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT      280 /note= "Encoded by GAC of the inverse complementary
FT      strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT      281 /note= "Encoded by GAA of the inverse complementary
FT      strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT      282 /note= "Encoded by TTC of the inverse complementary
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FT      283 /note= "Encoded by TTT of the inverse complementary
FT      strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT      284 /note= "Encoded by AAA of the inverse complementary
FT      strand of the sequence shown as SEQ ID NO:8 (AAD33068) "

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FT      285 /note= "Encoded by GAG of the inverse complementary
FT      strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT      286 /note= "Encoded by TAA of the inverse complementary
FT      strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT      287 /note= "Encoded by GAA of the inverse complementary
FT      strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT      288 /note= "Encoded by TTA of the inverse complementary
FT      strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT      289 /note= "Encoded by GGG of the inverse complementary
FT      strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT      290 /note= "Encoded by TTC of the inverse complementary
FT      strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT      291 /note= "Encoded by TCT of the inverse complementary
FT      strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT      292 /note= "Encoded by CCG of the inverse complementary
FT      strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT      293 /note= "Encoded by TGA of the inverse complementary
FT      strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT      294 /note= "Encoded by TGC of the inverse complementary
FT      strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT      295 /note= "Encoded by AAT of the inverse complementary
FT      strand of the sequence shown as SEQ ID NO:8 (AAD33068) "

```

MO200210402-A2.

07-FEB-2002.

30-JUL-2001; 2001WO-US023981.

28-JUL-2000; 2000US-0221860P.

(CHTR) CHIRON CORP.

Sun T, Feng J, Reinhard C, Fanli WJ, Williams LT;

WPI: 2002-206192/26.

N-PsDB; AAD30398, AAD33068.

Isolated nucleic acids encoding the human and Drosophila dishevelled associated kinase, referred to as PAR-1 kinase, useful for identifying PT modulators which can be used for modulating, inhibiting or preventing the growth of cancer cells.

Claim 7, Page 286-288; 297pp; English.

The invention relates to Dishevelled (Dsh) associated kinase, referred to as PAR-1 kinase in Drosophila and human homologues of PAR-1 referred to as PAR-1 α , PAR-1 β (alpha and beta) and PAR-1 γ . The invention also provides nucleic acid molecules encoding such proteins. PAR-1 activates the Wnt pathway and is required for Wnt signalling in mammalian cells. The PAR-1 modulators can be used to reduce the expression and/or biological activity of PAR-1. They are useful for modulating, inhibiting or preventing the growth of cancer cells. They are also useful for treating other diseases of hyperproliferation. Sequences of the invention are used in antisense therapy. The present sequence is human PAR-1 β beta protein.

Sequence 724 AA;

Query Match 100.0%; Score 3736; DB 5; Length 724;

Best Local Similarity 99.9%; Pred. NO. 6.3e-253; Matches 723; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 MSARTEPLTINERDEQPTLGHLSKPSKSNMIRNSATSADQPHIGNYRLTKTIG 60

Db 1 MSARPTPLPTLNERTDEQPTLGHLDSPKSSKSNMIRGNSATSADQPHIGNRYLLKTIG 60
Qy 61 KGNPAKYKLARHILITGKEVAVKIIDKTQLNSSSIQKLFREVRIMKVLNHPNIVLFEVIE 120
Db 61 KGNPAKYKLARHILITGKEVAVKIIDKTQLNSSSIQKLFREVRIMKVLNHPNIVLFEVIE 120
Qy 121 TEKTLVYVMEYASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYCHOKFTVHDLKAEN 180
Db 121 TEKTLVYVMEYASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYCHOKFTVHDLKAEN 180
Qy 181 LLLDADNMNIKIADFGFSNEFTFGNKLDTFCGSPPYAAPLPEFGKKYDGPVDVMSLGVIL 240
Db 181 LLLDADNMNIKIADFGFSNEFTFGNKLDTFCGSPPYAAPLPEFGKKYDGPVDVMSLGVIL 240
Qy 241 YTLVSGSLPPDGOQLKELRERVLRGKYRIPFYMSDTCENILKKFLINPSKRGTLQIOMK 300
Db 241 YTLVSGSLPPDGOQLKELRERVLRGKYRIPFYMSDTCENILKKFLINPSKRGTLQIOMK 300
Qy 301 DRMMNVGHEDDELKPYVEPLPDYKDPRTTELMSMGYTRBEEIQDSLVGQRVNEVMATYLL 360
Db 301 DRMMNVGHEDDELKPYVEPLPDYKDPRTTELMSMGYTRBEEIQDSLVGQRVNEVMATYLL 360
Qy 361 LGYKSSLEBDTITTLKRPSPADLTNNSAPSPSHKVQSVSANPKORRPSDQAPALPTSN 420
Db 361 LGYKSSLEBDTITTLKRPSPADLTNNSAPSPSHKVQSVSANPKORRPSDQAPALPTSN 420
Qy 421 SYSKKTQSNNAENKRPREDRESGRKASTAKVPSPLPGLERKTTTPTSTNSVLSTSTN 480
Db 421 SYSKKTQSNNAENKRPREDRESGRKASTAKVPSPLPGLERKTTTPTSTNSVLSTSTN 480
Qy 481 RSRNSPLLERASLGQASIQNGKDSIAFORVVASPSAMNIISSSGADRTNFPGVSSRS 540
Db 481 RSRNSPLLERASLGQASIQNGKDSIAFORVVASPSAMNIISSSGADRTNFPGVSSRS 540
Qy 541 TFHAGQLRQVRDQNLPEYVTPASPSPSGHSGRGAASISFQKTSKFRRLNLPESKDR 600
Db 541 TFHAGQLRQVRDQNLPEYVTPASPSPSGHSGRGAASISFQKTSKFRRLNLPESKDR 600
Qy 601 VETLRPHVVGSGGNDKKEKFEKAKPRSLRTWSMKTSSMEPEMMREIRKVLIDANSQ 660
Db 601 VETLRPHVVGSGGNDKKEKFEKAKPRSLRTWSMKTSSMEPEMMREIRKVLIDANSQ 660
Qy 661 SELHEKMLCMHGTPEGHEDFVQWEMEVCKLPRLSLNGVRFKRIISGTSMAFKNIASKIAN 720
Db 661 SELHEKMLCMHGTPEGHEDFVQWEMEVCKLPRLSLNGVRFKRIISGTSMAFKNIASKIAN 720
Qy 721 ELKUL 724
Db 721 ELKUL 724
RESULT 6
ABR43968 ID ABR43968 standard; protein; 777 AA.
XX ABR43968;
XX
XX 11-AUG-2003 (first entry)
XX
XX Human serine/threonine protein kinase.
XX
XX Serine/threonine protein kinase; cytosolic; antidiabetic; nootropic;
XX neuroprotective; antiinflammatory; analgesic; gene therapy; human;
XX chromosome 11q12-q13; enzyme.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX
XX MISC-difference 558 /note= "the corresponding DNA encodes a residue which is
XX FT not indicated in the present sequence"
XX
XX PN MO2003033708-A2.

XX
PD 24-Apr-2003.
XX
PF 14-OCT-2002; 2002MO-EP011478.
XX
PR 15-OCT-2001; 2001US-0328804P.
PR 27-FEB-2002; 2002US-0359688P.
PR 01-JUL-2002; 2002US-0392365P.
XX
PA (FARB) BAYER AG.
XX
PI Koehler RH;
XX
DR WPI: 2003-403226/38.
DR N-PSDB; ACC48106.
XX
XX
XX New polynucleotide encoding a serine/threonine protein kinase
XX polypeptide, useful for preventing, ameliorating or treating diseases
XX PT associated with the protein kinase dysfunction, e.g. cancer, diabetes or
XX PT a CNS disorder.
XX
XX Example 2; Page 167-169; 175pp; English.
XX
XX The invention relates to human serine/threonine protein kinase
XX CC polypeptide and encoding polynucleotides. The polypeptides can be
XX expressed by standard recombinant methodology. The polynucleotide and
XX CC polypeptide are useful in preventing, ameliorating or treating diseases
XX CC associated with serine/threonine protein kinase dysfunction. The diseases
XX CC include cancer, diabetes, a CNS disorder or chronic obstructive pulmonary
XX CC disease. These can also be used to treat pain associated with the above
XX CC disorders. The protein kinase is also used in various diagnostic assays
XX CC or in genetic testing. The present sequence represents a human serine/
XX CC threonine protein kinase
XX
SQ Sequence 777 AA;
Query Match 99.0%; Score 3700.5; DB 6; Length 777;
Best Local Similarity 93.2%; Pred. No. 2.2e-250;
Matches 724; Conservative 0; Mismatches 0; Indels 53; Gaps 1;
Qy 1 MSARPTPLPTLNERTDEQPTLGHLDSPKSSKSNMIRGNSATSADQPHIGNRYLLKTIG 60
Db 1 MSARPTPLPTLNERTDEQPTLGHLDSPKSSKSNMIRGNSATSADQPHIGNRYLLKTIG 60
Qy 61 KGNPAKYKLARHILITGKEVAVKIIDKTQLNSSSIQKLFREVRIMKVLNHPNIVLFEVIE 120
Db 61 KGNPAKYKLARHILITGKEVAVKIIDKTQLNSSSIQKLFREVRIMKVLNHPNIVLFEVIE 120
Qy 121 TEKTLVYVMEYASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYCHOKFTVHDLKAEN 180
Db 121 TEKTLVYVMEYASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYCHOKFTVHDLKAEN 180
Qy 181 LLLDADNMNIKIADFGFSNEFTFGNKLDTFCGSPPYAAPLPEFGKKYDGPVDVMSLGVIL 240
Db 181 LLLDADNMNIKIADFGFSNEFTFGNKLDTFCGSPPYAAPLPEFGKKYDGPVDVMSLGVIL 240
Qy 241 YTLVSGSLPPDGOQLKELRERVLRGKYRIPFYMSDTCENILKKFLINPSKRGTLQIOMK 300
Db 241 YTLVSGSLPPDGOQLKELRERVLRGKYRIPFYMSDTCENILKKFLINPSKRGTLQIOMK 300
Qy 301 DRMMNVGHEDDELKPYVEPLPDYKDPRTTELMSMGYTRBEEIQDSLVGQRVNEVMATYLL 360
Db 301 DRMMNVGHEDDELKPYVEPLPDYKDPRTTELMSMGYTRBEEIQDSLVGQRVNEVMATYLL 360
Qy 361 LGYKSSLEBDTITTLKRPSPADLTNNSAPSPSHKVQSVSANPKORRPSDQAPALPTSN 420
Db 361 LGYKSSLEBDTITTLKRPSPADLTNNSAPSPSHKVQSVSANPKORRPSDQAPALPTSN 420
Qy 421 SYSKKTQSNNAENKRPREDRESGRKASTAKVPSPLPGLERKTTTPTSTNSVLSTSTN 480
Db 421 SYSKKTQSNNAENKRPREDRESGRKASTAKVPSPLPGLERKTTTPTSTNSVLSTSTN 480
Qy 481 RSRNSPLLERASLGQASIQNGKDS----- 504

```

Db      481 RSRNSPLLRASLGQASIQNGKDSLTPMGSPASTASAGAASAPROHOKMSASVHPN 540
Qy      505 -----TAPORVPVAPSAHANISSSGGAPDRTNPPRGVSSRSTFHAQL 547
Db      541 KASGLPPTESNCEVPRPTAPORVPVAPSAHANISSSGGAPDRTNPPRGVSSRSTFHAQL 600
Qy      548 ROVRDOQNLPGVTPASPSPGSHQGRGASGSI FSKFTSKFYRRNLNBPESKDRVETLAPH 607
Db      601 ROVRDOQNLPGVTPASPSPGSHQGRGASGSI FSKFTSKFYRRNLNBPESKDRVETLAPH 660
Qy      608 VVSGSGNDKEKEEFPEAKPRSLRFTWSMKTSSMEPNEMREIRKVLNANSCOSELHXY 667
Db      661 VVSGSGNDKEKEEFPEAKPRSLRFTWSMKTSSMEPNEMREIRKVLNANSCOSELHXY 720
Qy      668 MLLCMHGTPGHEDPVOWEMEVCKLPRLSLNGVRFKRISGTSMAFKNIASKIANELKL 724
Db      721 MLLCMHGTPGHEDPVOWEMEVCKLPRLSLNGVRFKRISGTSMAFKNIASKIANELKL 777

```

RESULT 7

ABR43967
ID ABR43967 standard; protein; 780 AA.

XX ABR43967;

DT 11-AUG-2003 (first entry)

DE Human serine/threonine protein kinase.

XX Serine/threonine protein kinase; cytosolic; antidiabetic; noctropic;
KW neuropeptide; antiinflammatory; analgesic; gene therapy; human;
KM chromosome 11q12-q13; enzyme.

OS Homo sapiens.

XX MO200303708-A2.

PN 24-APR-2003.

PF 14-OCT-2002; 2002WO-EP011478.

XX 15-OCT-2001; 2001US-0328804P.

PR 27-FEB-2002; 2002US-0356688P.

PR 01-JUL-2002; 2002US-0392365P.

XX (FARB) BAYER AG.

FA Koehler RH;

PI WPI: 2003-403226/38.

DR N-PSDB; ACC48105.

XX New polynucleotide encoding a serine/threonine protein kinase
PT polypeptide, useful for preventing, ameliorating or treating diseases
PT associated with the protein kinase dysfunction, e.g. cancer, diabetes or
PT a CNS disorder.

XX Claim 1; Page 163-165; 175pp; English.

PS The invention relates to human serine/threonine protein kinase
XX polypeptide and encoding polynucleotide. The polypeptide can be
CC expressed by standard recombinant methodology. The polynucleotide and
CC polypeptide are useful in preventing, ameliorating or treating diseases
CC associated with serine/threonine protein kinase dysfunction. The diseases
CC include cancer, diabetes, a CNS disorder or chronic obstructive pulmonary
CC disease. These can also be used to treat pain associated with the above
CC disorders. The protein kinase is also used in various diagnostic assays
CC or in genetic testing. The present sequence represents a human serine/
CC threonine protein kinase

SO Sequence 780 AA;

Query Match 99.0%; Score 3699; DB 6; Length 780;
Best Local Similarity 92.8%; Pred. No. 2,8e-250;
Matches 724; Conservative 0; Mismatches 0; Indels 56; Gaps 1;

```

Qy      1 MSSARPTPLTNRDPEOPLTGLDPSKSSKMTIRGRSATSADQPHIATYRLIKTTG 60
Db      1 MSSARPTPLTNRDPEOPLTGLDPSKSSKMTIRGRSATSADQPHIATYRLIKTTG 60
Qy      61 KGNFAVKLARHILTKEVAVKIIDKTQANSSSLQKLFREVAIMKVLNPNIVKLFVYE 120
Db      61 KGNFAVKLARHILTKEVAVKIIDKTQANSSSLQKLFREVAIMKVLNPNIVKLFVYE 120
Qy      121 TEKTLVLMWYASGGEVFYLVAKGMEKEKAPKRVQVSAVOYCHQKFIYHRDLKAEN 180
Db      121 TEKTLVLMWYASGGEVFYLVAKGMEKEKAPKRVQVSAVOYCHQKFIYHRDLKAEN 180
Qy      181 LLLDADNLIKIDPFGSNFTFGNKLDPFCGSPYAAPLPGKKYDDPEVDVMSLGYTL 240
Db      181 LLLDADNLIKIDPFGSNFTFGNKLDPFCGSPYAAPLPGKKYDDPEVDVMSLGYTL 240
Qy      241 YTLVSGSLPFDQNLKELEERVLRGKYRIPFYMSIDCENLLKFLILNPSKRGTLQIMK 300
Db      241 YTLVSGSLPFDQNLKELEERVLRGKYRIPFYMSIDCENLLKFLILNPSKRGTLQIMK 300
Qy      301 DRMMNVGHEDDELKPYVEPLPYKDPRTTELMVSGYTRBEI QDSLVCQRINEVATYLL 360
Db      301 DRMMNVGHEDDELKPYVEPLPYKDPRTTELMVSGYTRBEI QDSLVCQRINEVATYLL 360
Qy      361 LGYKSELEGDITTLKPRPSADLTNSAPSPSHKQSVSANPQORRPSDQAGPAIPTSN 420
Db      361 LGYKSELEGDITTLKPRPSADLTNSAPSPSHKQSVSANPQORRPSDQAGPAIPTSN 420
Qy      421 SYSKTQSNMANKPEEDRDSGRKASTAKVPASPLPGLERKKTPTPTSTNSVLSSTGN 480
Db      421 SYSKTQSNMANKPEEDRDSGRKASTAKVPASPLPGLERKKTPTPTSTNSVLSSTGN 480
Qy      481 RSRNSPLLRASLGQASIQNGKDSLTPMGSPASTASAGAASAPROHOKMSASVHPN 540
Db      481 RSRNSPLLRASLGQASIQNGKDSLTPMGSPASTASAGAASAPROHOKMSASVHPN 540
Qy      505 -----TAPORVPVAPSAHANISSSGGAPDRTNPPRGVSSRSTFHA 544
Db      541 KASGLPPTESNCEVPRPTAPORVPVAPSAHANISSSGGAPDRTNPPRGVSSRSTFHA 600
Qy      545 GOLROVRDOQNLPGVTPASPSPGSHQGRGASGSI FSKFTSKFYRRNLNBPESKDRVETL 604
Db      601 GOLROVRDOQNLPGVTPASPSPGSHQGRGASGSI FSKFTSKFYRRNLNBPESKDRVETL 660
Qy      605 RPHVVGSGNDKEKEEFPEAKPRSLRFTWSMKTSSMEPNEMREIRKVLNANSCOSELH 664
Db      661 RPHVVGSGNDKEKEEFPEAKPRSLRFTWSMKTSSMEPNEMREIRKVLNANSCOSELH 720
Qy      665 EKMVLLCMHGTPGHEDPVOWEMEVCKLPRLSLNGVRFKRISGTSMAFKNIASKIANELKL 724
Db      721 EKMVLLCMHGTPGHEDPVOWEMEVCKLPRLSLNGVRFKRISGTSMAFKNIASKIANELKL 780

```

RESULT 8
ADJ96619
ID ADJ96619 standard; protein; 787 AA.

XX ADJ96619;

DT 06-MAY-2004 (first entry)

DE Human calcium/calmodulin-dependent protein kinase MARK2 protein Segid 76.

XX kinase; human; SNP; single nucleotide polymorphism;
KW tyrosine protein kinase; serine/threonine protein kinase; PTK; SNK;
KW gene therapy; cancer; immune-related disease; cardiovascular disease;
KW brain; neuronal associated disease; metabolic; inflammatory disorder;
KW cytosolic; neuropeptide; immunomodulator; antiinflammatory; enzyme;
KW calcium/calmodulin-dependent protein kinase; MARK2.

XX Homo sapiens.
OS 72.
XX
XX Key Location/Qualifiers
FH Misc-difference 415
FT /note= "Wild type Ala substituted for Pro by single
nucleotide polymorphism"
XX
XX MO2004006838-A2.
XX
XX 22-JAN-2004.
XX
XX 15-JUL-2003; 2003WO-US021730.
XX
XX 15-JUL-2002; 2002US-0395632P.
XX
XX (BUGE-) SUGEN INC.
XX
XX Whyte D, Manning G, Caenepeel S;
PI WPI; 2004-122753/12.
DR N-PSDB; ADJ96553.
XX
XX New nucleic acid molecule encoding a kinase polypeptide, useful for
PT preparing a composition for treating diseases or disorders, e.g., cancer,
PT or neurological, immunological or inflammatory disorders.
XX
XX Claim 1; SEQ ID NO 76; 366bp; English.
XX
XX This invention relates to a novel isolated, enriched or purified nucleic
CC acid molecule that encodes a kinase polypeptide. Specifically, it relates
CC to human tyrosine and serine/threonine protein kinases (PTK's and STK's),
CC as well as protein kinase-like enzymes. The present invention describes
CC screening methods to identify agonists, antagonists and antibodies that
CC can be used to modulate the activity or function of the mammalian kinase
CC enzymes. As such, these compositions can be used for gene therapy
CC purposes to treat diseases or disorders including cancer, immune-related
CC diseases, cardiovascular disease, brain or neuronal associated disease,
CC metabolic and inflammatory disorders. Accordingly, they exhibit
CC cytoprotective, neuroprotective, immunomodulator and antiinflammatory
CC activities. This polypeptide sequence is a human kinase protein sequence
CC of the invention.
XX
XX Sequence 767 AA;
60
Query Match 98.2%; Score 3670.5; DB 8; Length 787;
Best Local Similarity 91.6%; Pred. No. 2.8e-248;
Matches 721; Conservative 1; Mismatches 2; Indels 63; Gaps 2;
QY 1 MSSARTPLPTLNEDTQPTLGHLDSPSSKSNMIRGNATSADDEPHIGNYFLKTIG 60
DB 1 MSSARTPLPTLNEDTQPTLGHLDSPSSKSNMIRGNATSADDEPHIGNYFLKTIG 60
QY 61 KGNFAKYKLAARHILTGKEVAVKIIDKTOLNSSLQKLFREVRIMKVLNHPYIVLFEVIE 120
DB 61 KGNFAKYKLAARHILTGKEVAVKIIDKTOLNSSLQKLFREVRIMKVLNHPYIVLFEVIE 120
QY 121 TEKTLVLMVEYASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYCHQKPIVHBDLKAEN 180
DB 121 TEKTLVLMVEYASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYCHQKPIVHBDLKAEN 180
QY 121 TEKTLVLMVEYASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYCHQKPIVHBDLKAEN 180
DB 121 TEKTLVLMVEYASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYCHQKPIVHBDLKAEN 180
QY 181 LLLDADANNIKIADGFSNEPTFGNKLDTFGCSPPYAAPELFGKKYTGPEYDWSLGVIL 240
DB 181 LLLDADANNIKIADGFSNEPTFGNKLDTFGCSPPYAAPELFGKKYTGPEYDWSLGVIL 240
QY 181 LLLDADANNIKIADGFSNEPTFGNKLDTFGCSPPYAAPELFGKKYTGPEYDWSLGVIL 240
DB 181 LLLDADANNIKIADGFSNEPTFGNKLDTFGCSPPYAAPELFGKKYTGPEYDWSLGVIL 240
QY 241 YTLVSGSLPFDGQULKELEERVLGKXTRIPFYMTDCENILKKVLINPSSRGTLLEOIMK 300
DB 241 YTLVSGSLPFDGQULKELEERVLGKXTRIPFYMTDCENILKKVLINPSSRGTLLEOIMK 300
QY 301 DRMMNVGHEDEDELKPYVEPLPDYKDPRRTBLMWSMGYTRIEIODSLVGQRVNEVMATYLL 360
DB 301 DRMMNVGHEDEDELKPYVEPLPDYKDPRRTBLMWSMGYTRIEIODSLVGQRVNEVMATYLL 360

QY 361 LGYSSSELEGGDTITLKRPASADLTNSSAPSPSHKRVSVANPKORRPSDOAGPAIPTSN 420
DB 361 LGYSSSELEGGDTITLKRPASADLTNSSAPSPSHKRVSVANPKORRPSDOAGPAIPTSN 420
QY 421 SYSKKTOSNNAENRPEEDRESGRKASTAKVPASPGLERKKTPTPTSTNSVLTSTN 480
DB 421 SYSKKTOSNNAENRPEEDRESGRKASTAKVPASPGLERKKTPTPTSTNSVLTSTN 480
QY 481 RSRNSPLLEPASLIGQASIQNGKD----- 503
DB 481 RSRNSPLLEPASLIGQASIQNGKDLTWPGRASTPASAAVSAARPROHQKSMGASVHPN 540
QY 504 -----STAPQVPVAPSPSANNISSGCGADPRNFRGVSSRSTFPAQ 546
DB 541 KASGLPPTESNCEVPSTAPQVPVAPSPSANNISSGCGADPRNFRGVSSRSTFPAQ 600
QY 547 LRQVRDQONTPLYGTPASPGRHSQGRGASGSIPTSKFTSKFV-----RRYLNRPES 597
DB 601 LRQVRDQONTPLYGTPASPGRHSQGRGASGSIPTSKFTSKFVRNLSFRARRLNRPES 660
QY 598 KDRVETLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPNEMREIRKVLDAV 657
DB 661 KDRVETLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPNEMREIRKVLDAV 720
QY 658 SCQSELHEKTMLCMGTPEHEDPVQWEMEVCKLPRLSLNGVPRKRLSGTSMARKNTASK 717
DB 721 SCQSELHEKTMLCMGTPEHEDPVQWEMEVCKLPRLSLNGVPRKRLSGTSMARKNTASK 780
QY 718 IANELKL 724
DB 781 IANELKL 787
RESULT 9
ID ABR43965 standard; protein; 722 AA.
XX ABR43965
AC ABR43965;
XX
DT 11-AUG-2003 (first entry)
XX
DE Rat serine/threonine protein kinase MARK2.
XX
KM Serine/threonine protein kinase; cytoprotective; antidiabetic; nootropic;
KM neuroprotective; antiinflammatory; analgesic; gene therapy; rat; MARK2;
KM chromosome 11q12-q13; enzyme.
XX
OS Rattus norvegicus.
XX
FN WO2003033708-A2.
XX
PD 24-APR-2003.
XX
PF 14-OCT-2002; 2002WO-EP011478.
XX
PR 15-OCT-2001; 2001US-0328804P.
XX
PR 27-FEB-2002; 2002US-0359688P.
XX
PR 01-JUL-2002; 2002US-0392365P.
XX
PA (FARB) BAYER AG.
XX
XX Koehler RH;
XX
XX WPI; 2003-403226/38.
XX
PT New polynucleotide encoding a serine/threonine protein kinase
PT polypeptide, useful for preventing, ameliorating or treating diseases
PT associated with the protein kinase dysfunction, e.g. cancer, diabetes or
PT a CNS disorder.
XX
PS Disclosure; Fig 1; 175bp; English.
XX

CC The invention relates to human serine/threonine protein kinase
 CC polypeptide and encoding polynucleotides. The polypeptides can be
 CC expressed by standard recombinant methodology. The polynucleotide and
 CC polypeptide are useful in preventing, ameliorating or treating diseases
 CC associated with serine/threonine protein kinase dysfunction. The diseases
 CC include cancer, diabetes, a CNS disorder or chronic obstructive pulmonary
 CC disease. These can also be used to treat pain associated with the above
 CC disorders. The protein kinase is also used in various diagnostic assays
 CC or in genetic testing. The present sequence represents a rat serine/
 CC threonine protein kinase MARK2
 XX

Sequence 722 AA;

Query Match 97.8%; Score 3654; DB 6; Length 722;
 Best Local Similarity 97.8%; Pred. No. 3.5e-247;

Matches 708; Conservative 9; Mismatches 5; Indels 2; Gaps 1;

QY 1 MSSARTPLPTINERDTEOPTLGHLDSPSSKSNMIRGNSATSADQPHIGNYRLKLTIG 60
 DB 1 MSSARTPLPTINERDTEOPTLGHLDSPSSKSNMIRGNSATSADQPHIGNYRLKLTIG 60
 QY 61 KGNFAKVKLARHILTGKEVAVKIIDKTQLNSSSLQKLFREVRIMKVLNHPNIVKLFVIE 120
 DB 61 KGNFAKVKLARHILTGKEVAVKIIDKTQLNSSSLQKLFREVRIMKVLNHPNIVKLFVIE 120
 QY 121 TEKTLVLMVEYASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYCHQKFIHRDLKAEN 180
 DB 121 TEKTLVLMVEYASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYCHQKFIHRDLKAEN 180
 QY 121 TEKTLVLMVEYASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYCHQKFIHRDLKAEN 180
 DB 121 TEKTLVLMVEYASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYCHQKFIHRDLKAEN 180
 QY 181 LLLDADNMNIIKIDAFGFSNEFTFGNKLDTFCGSPPYAAPELFQGGKYDGPEVDVMSLGVIIL 240
 DB 181 LLLDADNMNIIKIDAFGFSNEFTFGNKLDTFCGSPPYAAPELFQGGKYDGPEVDVMSLGVIIL 240
 QY 241 YTLVSGSLPFDGQNLKELREVLNKGKRIIPFYMSDCEMLKKPLINPSKRGTLBEQIM 300
 DB 241 YTLVSGSLPFDGQNLKELREVLNKGKRIIPFYMSDCEMLKKPLINPSKRGTLBEQIM 300
 QY 301 DRWNVGHEDDELKPYVEPLPDYDOPRTEIMVSMGYTRREIQQSLVQGRYNEVMATYLL 360
 DB 301 DRWNVGHEDDELKPYVEPLPDYDOPRTEIMVSMGYTRREIQQSLVQGRYNEVMATYLL 360
 QY 301 DRWNVGHEDDELKPYVEPLPDYDOPRTEIMVSMGYTRREIQQSLVQGRYNEVMATYLL 360
 DB 301 DRWNVGHEDDELKPYVEPLPDYDOPRTEIMVSMGYTRREIQQSLVQGRYNEVMATYLL 360
 QY 361 LGYSSSELEGGDTITLKRPSADLTNSSAPSPSHVQSVSANPKQRFSPQAGPAIPTS 420
 DB 361 LGYSSSELEGGDTITLKRPSADLTNSSAPSPSHVQSVSANPKQRFSPQAGPAIPTS 420
 QY 421 SYSKTOSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLSTSTY 480
 DB 421 SYSKTOSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLSTSTY 480
 QY 481 RSRNSPLLEPASLGQASTONGKSTAFQRPVVASPSAHNITSSSGCAPDRTNPRGVSSRS 540
 DB 481 RSRNSPLLEPASLGQASTONGKSTAFQRPVVASPSAHNITSSSGCAPDRTNPRGVSSRS 540
 QY 479 RSRNSPLLEPASLGQASTONGKSTAFQRPVVASPSAHNITSSSGCAPDRTNPRGVSSRS 538
 DB 479 RSRNSPLLEPASLGQASTONGKSTAFQRPVVASPSAHNITSSSGCAPDRTNPRGVSSRS 538
 QY 541 TFHAGQLROYDQONLTVYGTVPASPSGHSQGRGASGISKTSKTSFVRNINLEPSSK 600
 DB 541 TFHAGQLROYDQONLTVYGTVPASPSGHSQGRGASGISKTSKTSFVRNINLEPSSK 600
 QY 539 TFHAGQLROYDQONLTVYGTVPASPSGHSQGRGASGISKTSKTSFVRNINLEPSSK 598
 DB 539 TFHAGQLROYDQONLTVYGTVPASPSGHSQGRGASGISKTSKTSFVRNINLEPSSK 598
 QY 601 VETLRPHVVSQGDNDKEKEPRKAPRSILFTWSMKTSSMEBENMRIRKVLANDNSQ 660
 DB 601 VETLRPHVVSQGDNDKEKEPRKAPRSILFTWSMKTSSMEBENMRIRKVLANDNSQ 660
 QY 599 VETLRPHVVSQGDNDKEKEPRKAPRSILFTWSMKTSSMEBENMRIRKVLANDNSQ 658
 DB 599 VETLRPHVVSQGDNDKEKEPRKAPRSILFTWSMKTSSMEBENMRIRKVLANDNSQ 658
 QY 661 SEIHEKMTLCMHGTPEHDFVQMEMEVCLPRLSLINGVRFKRIISTSWAFKILASKIAN 720
 DB 661 SEIHEKMTLCMHGTPEHDFVQMEMEVCLPRLSLINGVRFKRIISTSWAFKILASKIAN 720
 QY 659 SEIHEKMTLCMHGTPEHDFVQMEMEVCLPRLSLINGVRFKRIISTSWAFKILASKIAN 718
 DB 659 SEIHEKMTLCMHGTPEHDFVQMEMEVCLPRLSLINGVRFKRIISTSWAFKILASKIAN 718
 QY 721 ELKFL 724
 DB 719 ELKFL 722

RESULT 10
 ADI30083
 ID ADI30083 standard; protein; 722 AA.

XX ADI30083;
 AC 22-Apr-2004 (first entry)
 DT Rat serine/threonine kinase protein.
 XX
 DE kinase; serine/threonine kinase; immune response; drug screening;
 KW tissue typing; pharmacogenomic analysis; tumour;
 KW brain anaplastic oligodendroglioma; lung carcinoma tissue;
 KW soft tissue leiomyosarcoma; gene therapy; transgenic animal; cytostatic;
 KW Rat; enzyme.
 XX
 OS Rattus norvegicus.
 XX
 PN US2003232408-A1.
 XX 18-DEC-2003.
 XX
 PF 21-OCT-2002; 2002US-00274194.
 XX
 PR 31-OCT-2001; 2001US-00984890.
 XX
 PA (APPL-) APPLERA CORP.
 PI Van C, Li Z, Neelam B, Difrancesco V, Beasley EM;
 PI WPI; 2004-061277/06.
 DR
 XX
 PS New peptides related to kinase protein subfamily useful for treating
 PT disorders associated with abnormal expression of kinase protein in
 PT testis, nervous tissue, fetal, lung, ovary tumor tissue.
 XX
 XX Disclosure; SEQ ID NO 4; 111pp; English.

CC The invention relates to human kinase protein related to serine/threonine
 CC kinase subfamily and its corresponding nucleic acid sequence. The
 CC invention is useful to raise antibodies or to elicit immune response, as
 CC reagents in assays to determine the levels of protein in biological
 CC fluids, and as markers for tissues where the corresponding protein is
 CC expressed. It is also useful in drug screening assays, tissue typing and
 CC pharmacogenomic analysis. The sequences of the invention are useful in
 CC treating disorders associated with the absence of, inappropriate, or
 CC unwanted expression of kinase protein in testis, nervous tissue, foetal,
 CC lung, brain anaplastic oligodendroglioma, lung carcinoma tissue, soft
 CC tissue leiomyosarcoma, ovary tumour tissue, or germ cell tumour tissue.
 CC These are also useful in gene therapy and are useful as models for the
 CC development of human therapeutic targets, aid in the identification of
 CC therapeutic proteins and serve as targets for the development of human
 CC therapeutic agents that modulate protease activity in cells and tissues
 CC that express the kinase peptide. The host cells are useful in producing a
 CC kinase protein or peptide, and non-human transgenic animals. The present
 CC sequence is rat serine/threonine kinase protein.

Sequence 722 AA;

Query Match 97.8%; Score 3654; DB 8; Length 722;
 Best Local Similarity 97.8%; Pred. No. 3.5e-247;

Matches 708; Conservative 9; Mismatches 5; Indels 2; Gaps 1;

QY 1 MSSARTPLPTINERDTEOPTLGHLDSPSSKSNMIRGNSATSADQPHIGNYRLKLTIG 60
 DB 1 MSSARTPLPTINERDTEOPTLGHLDSPSSKSNMIRGNSATSADQPHIGNYRLKLTIG 60
 QY 61 KGNFAKVKLARHILTGKEVAVKIIDKTQLNSSSLQKLFREVRIMKVLNHPNIVKLFVIE 120
 DB 61 KGNFAKVKLARHILTGKEVAVKIIDKTQLNSSSLQKLFREVRIMKVLNHPNIVKLFVIE 120
 QY 121 TEKTLVLMVEYASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYCHQKFIHRDLKAEN 180
 DB 121 TEKTLVLMVEYASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYCHQKFIHRDLKAEN 180
 QY 121 TEKTLVLMVEYASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYCHQKFIHRDLKAEN 180
 DB 121 TEKTLVLMVEYASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYCHQKFIHRDLKAEN 180
 QY 181 LLLDADNMNIIKIDAFGFSNEFTFGNKLDTFCGSPPYAAPELFQGGKYDGPEVDVMSLGVIIL 240

Db 181 LLLDADNMNLIKADPGFSNEFTFGNKLDTFCGSPPYAAPELFOGKXYGPEVDWMSLVIL 240
Qy 241 YTLVSGSLPFDGQNLKELREVRVLRGKTRIPFYMTSDCNLLKFLILNPSKRGTLBOIMK 300
Db 241 YTLVSGSLPFDGQNLKELREVRVLRGKTRIPFYMTSDCNLLKFLILNPSKRGTLBOIMK 300
Qy 301 DRMMNVGHEDDELKPYEPLPDYKDPRTTELVMWSGTYREIIODSLVGQRVNEVMATYLL 360
Db 301 DRMMNVGHEDDELKPYEPLPDYKDPRTTELVMWSGTYREIIODSLVGQRVNEVMATYLL 360
Qy 361 LGYKSSLEBDTTLTKRPSADLTNSSAPSPSHKVRQSVANPKQRSPDQAPAIPTSN 420
Db 361 LGYKSSLEBDTTLTKRPSADLTNSSAPSPSHKVRQSVANPKQRSPDQAPAIPTSN 420
Qy 421 SYSKKTOSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTTPPTSTNSVLSTSTN 480
Db 421 SYSKKTOSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTTPPTSTNSVLSTSTN 480
Qy 481 RSRNSPLERASIGQASIONGKOSTAPORVPVAPSAHNISSSGADPRTNPPRGVSSRS 540
Db 479 RSRNSPLERASIGQASIONGKOSTAPORVPVAPSAHNISSSGADPRTNPPRGVSSRS 538
Qy 541 TFHAGQLRQVRDQNLPGYVTPASPSPSGHSGRGAAGSIFSKFTSKFVRRLNLEPESKDR 600
Db 539 TFHAGQLRQVRDQNLPGYVTPASPSPSGHSGRGAAGSIFSKFTSKFVRRLNLEPESKDR 598
Qy 601 VETLRPHVVGSGNDKEKEKEFEAKPRSLRFTWSMKTTSMEPNEMREIRKVLANSQC 660
Db 599 VETLRPHVVGSGNDKEKEKEFEAKPRSLRFTWSMKTTSMEPNEMREIRKVLANSQC 658
Qy 661 SELHEKTMLLCMGTPEGHEDPVOEMEVCKLPRLSLNGVAFKRLSGTSMAPKXIASKIAN 720
Db 659 SELHEKTMLLCMGTPEGHEDPVOEMEVCKLPRLSLNGVAFKRLSGTSMAPKXIASKIAN 718
Qy 721 ELKL 724
Db 719 ELKL 722

RESULT 11
AD060238
ID AD060238 standard; protein; 722 AA.
AC AD060238;
XX
DT 07-OCT-2004 (first entry)
XX
DE Rat serine/threonine kinase.
XX
KW allelic variant; orthologue; therapeutic; kinase activity modulation;
KW kinase associated disorder; rat; kinase;
KW serine/threonine kinase subfamily; enzyme.
XX
OS Rattus norvegicus.
XX
PN US2004137499-A1.
PD 15-JUL-2004.
PE 21-JAN-2004; 2004US-00760407.
PR 31-OCT-2001; 2001US-00984890.
PR 21-OCT-2002; 2002US-00274194.
XX
PA (APPL-) APPLERA CORP.
PI Van C, Li Z, Neelam B, Diffrancesco V, Beasley EM,
XX
DR WPI, 2004-533359/51.
XX
PT New isolated human kinase peptide, useful for developing human
therapeutic targets, identifying therapeutic proteins, or as targets for

PT developing human therapeutic agents that modulate kinase activity in
cells and tissues.
XX
PS Disclosure, SEQ ID NO 4, 11pp, English.
XX
CC The invention describes an isolated peptide (1). The peptide comprises an
CC amino acid sequence selected from: an amino acid sequence comprising 724
CC of SEQ ID NO. 2, where the allelic variant is encoded by a nucleic acid
CC molecule that hybridizes to the opposite strand of a nucleic acid
CC molecule comprising 2175 bp (SEQ ID NO. 1) or 7595 bp (SEQ ID NO. 3); an
CC amino acid sequence of an orthologue of SEQ ID NO. 2, where the
CC orthologue is encoded by a nucleic acid molecule that hybridizes to the
CC opposite strand of SEQ ID NO. 1 or 3; or a fragment of SEQ ID NO. 2,
CC where the fragment comprises at least 10 contiguous amino acids. The
CC peptide sequence can be used as models for the development of human
CC therapeutic targets, aid in the identification of therapeutic proteins,
CC and serve as targets for the development of human therapeutic agents that
CC modulate kinase activity in cells and tissues and express the kinase.
CC They can also be used for biological assays related to kinases, in drug
CC screening assays in cell-based, or cell-free systems. It can also be used
CC to screen a compound for the ability to stimulate or inhibit interaction
CC between the kinase proteins and a molecule that normally interacts with
CC the kinase protein. They can also be used as targets for diagnosing a
CC disease or predisposition to disease mediated by the peptide, and for
CC treating disorders with an absence of, inappropriate, or unwanted
CC expression of the protein. This is the amino acid sequence of a rat
CC serine/threonine kinase used in a comparison with the human kinase of the
XX invention.
SQ Sequence 722 AA:
Query Match 97.8%; Score 3654; DB 8; Length 722;
Best Local Similarity 97.8%; Pred. No. 3,5e-247;
Matches 708; Conservative 9; Mismatches 5; Indels 2; Gaps 1;
Qy 1 MSSARPTLPNTNEDTOPTLGHLSKPSKSMIRGNATSDADPHGNRLTKTG 60
Db 1 MSSARPTLPNTNEDTOPTLGHLSKPSKSMIRGNATSDADPHGNRLTKTG 60
Qy 61 KGNFAVKLARHILITGEVAVKIIDKTOLNSSLSQKLFRVRIIMKVLNHPNIVKLFVIE 120
Db 61 KGNFAVKLARHILITGEVAVKIIDKTOLNSSLSQKLFRVRIIMKVLNHPNIVKLFVIE 120
Qy 121 TEKTLVLYMEYASGGEVFDVLVHGRMKKEAPAKRQVAVQYCHQKFIYHDLKAEN 180
Db 121 TEKTLVLYMEYASGGEVFDVLVHGRMKKEAPAKRQVAVQYCHQKFIYHDLKAEN 180
Qy 181 LLLDADNMNLIKADPGFSNEFTFGNKLDTFCGSPPYAAPELFOGKXYGPEVDWMSLVIL 240
Db 181 LLLDADNMNLIKADPGFSNEFTFGNKLDTFCGSPPYAAPELFOGKXYGPEVDWMSLVIL 240
Qy 241 YTLVSGSLPFDGQNLKELREVRVLRGKTRIPFYMTSDCNLLKFLILNPSKRGTLBOIMK 300
Db 241 YTLVSGSLPFDGQNLKELREVRVLRGKTRIPFYMTSDCNLLKFLILNPSKRGTLBOIMK 300
Qy 301 DRMMNVGHEDDELKPYEPLPDYKDPRTTELVMWSGTYREIIODSLVGQRVNEVMATYLL 360
Db 301 DRMMNVGHEDDELKPYEPLPDYKDPRTTELVMWSGTYREIIODSLVGQRVNEVMATYLL 360
Qy 361 LGYKSSLEBDTTLTKRPSADLTNSSAPSPSHKVRQSVANPKQRSPDQAPAIPTSN 420
Db 361 LGYKSSLEBDTTLTKRPSADLTNSSAPSPSHKVRQSVANPKQRSPDQAPAIPTSN 420
Qy 421 SYSKKTOSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTTPPTSTNSVLSTSTN 480
Db 421 SYSKKTOSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTTPPTSTNSVLSTSTN 478
Qy 481 RSRNSPLERASIGQASIONGKOSTAPORVPVAPSAHNISSSGADPRTNPPRGVSSRS 540
Db 479 RSRNSPLERASIGQASIONGKOSTAPORVPVAPSAHNISSSGADPRTNPPRGVSSRS 538
Qy 541 TFHAGQLRQVRDQNLPGYVTPASPSPSGHSGRGAAGSIFSKFTSKFVRRLNLEPESKDR 600

PI Hatella A7A, Emerling BM, Kable AE, Richardson TW, Becha SD;
PI Baughn MR, Tang YT, Jai PG, Lee SJ, Griffin JA, Khare R;
PI Elliott VA, Jin P, Hawkins PR, Swarnkar A, Chawla NK, Tiran UK;
PI Gunaratna R, Ding L, Margulis JP, Thornton MB, Forsythe LJ, Lee BA;
PI Gietzen KJ, Ramkumar J;
XX MPI, 2004-132950/13.
DR N-PSDB, ADI40929.
XX
PT New human kinases and phosphatases, useful for diagnosing, treating or
PT preventing atherosclerosis, hypertension, AIDS, allergy, multiple
PT sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer
PT or hepatitis.
XX
PS Claim 1; SEQ ID NO 42; 330bp; English.
XX
CC The present sequence represents a human kinase and phosphatase (KPP)
CC protein. KPP sequences have cardiovascular, antiarteriosclerotic,
CC hypotensive, vasotropic, antiinflammatory, antiangiinal, anti-HIV,
CC antiallergic, antidiabetic, immunosuppressive, antihydroid,
CC dermatological, antidiabetic, nephrotoxic, antigout, gastrointestinal,
CC neuroprotective, osteopathic, antirheumatic, uropathic, ophthalmological,
CC antineumatic, antiparkinsonian, nootropic, anticonvulsant, hepatotropic,
CC CNS, antipsoriatic, haemostatic, cytosolic, antilipemic, antiparasitic,
CC antihelminthic, antibacterial, virucide, protozoacide and fungicide
CC activities, and can be used in gene therapy, and as kinase modulators and
CC phosphatase modulators. KPP proteins, polynucleotides, agonists and
CC antagonists can be used for diagnosing, treating or preventing disorders
CC associated with aberrant expression of KPP, such as cardiovascular
CC diseases (e.g. atherosclerosis, hypertension, vasculitis, angina pectoris
CC or congestive heart failure), immune system disorders (e.g. AIDS,
CC allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's
CC disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome,
CC gout, irritable bowel syndrome, multiple sclerosis, osteoarthritis,
CC osteoporosis, pancreatitis, Reiter's syndrome, rheumatoid arthritis,
CC Sjogren's syndrome or uveitis), neurological disorders (e.g. Alzheimer's
CC disease, Parkinson's disease, Huntington's disease, dementia or
CC epilepsy), disorders affecting growth and development (e.g. cirrhosis,
CC hepatitis, mixed connective tissue disease, psoriasis or primary
CC thrombocytopenia), cell proliferative disorders (e.g.
CC hypercholesterolaemia, hyperlipidaemia or cancer), or viral, bacterial,
CC fungal, parasitic, protozoan or helminthic infections. The KPP and
CC polynucleotides are also useful in assessing the effects of exogenous
CC compounds on the expression of nucleic acids and kinases and
CC phosphatases, or for facilitating the drug discovery process, including
CC determination of efficacy, dosage, toxicity and pharmacology. The
CC polynucleotides encoding KPP are useful for creating transgenic animals
CC to model human disease.
XX
XX Sequence 799 AA;
SQ

Query Match 96.1%; Score 3589.5; DB 8; Length 799;
Best Local Similarity 88.7%; Pred. No. 1.3e-242;
Matches 709; Conservative 4; Mismatches 11; Indels 75; Gaps 3;

QY 1 MSSARTPLPTL-----NERDTEOPTGLHDSKPSKSMIRGRNS 40
DB 1 MEVAGSPFPPLQSVACILTLAHPAVGNILQHRRRAGPTLGLHDSKPSKSMIRGRNS 60
QY 41 ATSADHOPHTGNRLKTGKGNFAVKLARHILTEKEVAVKIIDKTQUNSSSLQTLFPE 100
DB 61 ATSADHOPHTGNRLKTGKGNFAVKLARHILTEKEVAVKIIDKTQUNSSSLQTLFPE 120
QY 101 VRIIMKVLNPNIVKLEFEVETEKTLYLWMEYASGSEVPDYLVAHGMRKEKARAKPROV 160
DB 121 VRIIMKVLNPNIVKLEFEVETEKTLYLWMEYASGSEVPDYLVAHGMRKEKARAKPROV 180
QY 161 SAVOYCHOKFYIHRDIKAENLLIDADMMIKIADPGFSNEFTGKLTDFCGSPYAAPBL 220
DB 181 SAVOYCHOKFYIHRDIKAENLLIDADMMIKIADPGFSNEFTGKLTDFCGSPYAAPBL 240
QY 221 FQGGKYDGEVDVWSLGVILLYTLVSGSLPFDQNLKEILERVLRGKRYRPFYMSIDCENL 280

DB 241 FQGGKYDGEVDVWSLGVILLYTLVSGSLPFDQNLKEILERVLRGKRYRPFYMSIDCENL 300
QY 281 LKKEFLILNPSKGTLEQIMKDRMNVVGHEDDELKPYVEPLPYKOPRRTLELWVSMGYTR 340
DB 301 LKKEFLILNPSKGTLEQIMKDRMNVVGHEDDELKPYVEPLPYKOPRRTLELWVSMGYTR 360
QY 341 EIODSLVQGRVNEWATYLLILGYKSELEKGDITTLKPRPSADLTNNSAPSPSHKYQSV 400
DB 361 EIODSLVQGRVNEWATYLLILGYKSELEKGDITTLKPRPSADLTNNSAPSPSHKYQSV 420
QY 401 ANPKORFSDQ-AGPAIPTNSYSKKTOSNNENRPEEDRSGRKAATAVPASPLPG 459
DB 421 ANPKORFSDQAGPAIPTNSYSKKTOSNNENRPEEDRSGRKAATAVPASPLPG 480
QY 460 LERKKTTPPTSTNSVLTSTNSRNSPLLERASLQASIQNGKD----- 503
DB 481 LERKKTTPPTSTNSVLTSTNSRNSPLLERASLQASIQNGKDLTMPGRASATASASA 540
QY 504 -----STAPQVPVAPSPAHNISSGCG 525
DB 541 AVSAARPRQHKMSASVHPNKAAGLPTESNCEVPRPSTAPQVPVAPSPAHNISSGCG 600
QY 526 APPRTNPPRGVSRSTFPAQOLROYRDOONLPYGTVPASPSGSGRGAAGSIFSKPTS 585
DB 601 APPRTNPPRGVSRSTFPAQOLROYRDOONLPYGTVPASPSGSGRGAAGSIFSKPTS 660
QY 586 KTVRRNLNPESSKDVETLIRPHVVGSGNDKEKEFEAKPRSLRFTWSMKTSSMEPNE 645
DB 661 KTVRRNLNPESSKDVETLIRPHVVGSGNDKEKEFEAKPRSLRFTWSMKTSSMEPNE 720
QY 646 MREIRKVLNANSCOSELHEKYMILLCMGTGCHEDPFQWMEVCKLPLSLNGVRFKIS 705
DB 721 MREIRKVLNANSCOSELHEKYMILLCMGTGCHEDPFQWMEVCKLPLSLNGVRFKIS 780
QY 706 GTSMAFKNIASKIANELKL 724
DB 781 GTSMAFKNIASKIANELKL 799

RESULT 15
AAE19050
ID AAE19050 standard; protein; 691 AA.
XX
AC AAE19050;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human PAR-1B alpha protein.
XX
KW Human; Dishevelled associated kinase; PAR-1 kinase; enzyme; PAR-1A;
KW PAR-1B alpha; PAR-1B beta; PAR-1C; cancer; hyperproliferative disease;
KW antisense therapy; Dsh.
XX
OS Homo sapiens.
XX
PN WO200210402-A2.
XX
PD 07-FEB-2002.
XX
PF 30-JUL-2001; 2001WO-US023981.
XX
PR 28-JUL-2000; 2000US-0221860P.
XX
PA (CHIR) CHIRON CORP.
XX
PI Sun T, Feng J, Reinhard C, Fantl WJ, Williams LT;
XX
DR MPI, 2002-206192/26.
XX
DR N-PSDB; AAD30397.
XX
PT Isolated nucleic acids encoding the human and Drosophila Dishevelled
PT associated kinase, referred to as PAR-1 kinase, useful for identifying
PT modulators which can be used for modulating, inhibiting or preventing the

PT growth of cancer cells.

XX
PS Claim 7, Page 283-284; 297pp; English.

CC The invention relates to Dishevelled (Dsh) associated kinase, referred to
CC as PAR-1 kinase in Drosophila and human homologues of PAR-1 referred to
CC as PAR-1a, PAR-1B (alpha and beta) and PAR-1c. The invention also
CC provides nucleic acid molecules encoding such proteins. PAR-1 activates
CC the Wnt pathway and is required for Wnt signaling in mammalian cells.
CC The PAR-1 modulators can be used to reduce the expression and/or
CC biological activity of PAR-1. They are useful for modulating, inhibiting
CC or preventing the growth of cancer cells. They are also useful for
CC treating other diseases of hyperproliferation. Sequences of the invention
CC are used in antisense therapy. The present sequence is human PAR-1B alpha
CC protein

XX
SQ Sequence 691 AA;

Query Match 95.4%; Score 3566; DB 5; Length 691;

Best Local Similarity 99.9%; Pred. No. 4.9e-241;

Matches 690; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 34 MIRGRNSATSADQPHIGNYRLKTTIGKNFAKYKLARHILTGKEVAVKIIDKTQLNSSS 93
DB 1 MIRGRNSATSADQPHIGNYRLKTTIGKNFAKYKLARHILTGKEVAVKIIDKTQLNSSS 60
QY 94 LQKLFREVRIMKVLNHNPIYKLPVITETKTLIYVMEYASGGEVFDYLVAHGRMKEKEAR 153
DB 61 LQKLFREVRIMKVLNHNPIYKLPVITETKTLIYVMEYASGGEVFDYLVAHGRMKEKEAR 120
QY 154 AKFRQVSAVOYCHQKTIYHRDLKAENLLDADNMIKIADFGSNEFTFGNKLDTFCGSP 213
DB 121 AKFRQVSAVOYCHQKTIYHRDLKAENLLDADNMIKIADFGSNEFTFGNKLDTFCGSP 180
QY 214 PYAAPELFOGKXYDGEVDVWSLGVILYTLVSGSLPFDGQNLKELRERVLRGKYRIPEYM 273
DB 181 PYAAPELFOGKXYDGEVDVWSLGVILYTLVSGSLPFDGQNLKELRERVLRGKYRIPEYM 240
QY 274 SFDCENLKKFLLINPSKRGTLQIMKORMNNGHEDDLKPYVEPLDYKDPRTETLMV 333
DB 241 STDCENLKKFLLINPSKRGTLQIMKORMNNGHEDDLKPYVEPLDYKDPRTETLMV 300
QY 334 SMGYTREIQLDSLVGQRYNEVMATYLLGYKSSLEGGDTTLKPRPSADLTNSAPSPSH 393
DB 301 SMGYTREIQLDSLVGQRYNEVMATYLLGYKSSLEGGDTTLKPRPSADLTNSAPSPSH 360
QY 394 KYGRSVSANPKORRFSQAGPAIPTNSYSKKTQSNNAENKRPEDRESGRKASTAKVP 453
DB 361 KYGRSVSANPKORRFSQAGPAIPTNSYSKKTQSNNAENKRPEDRESGRKASTAKVP 420
QY 454 ASPPLGLEERKKTPTPTSTNSVLSTNRSNPSLLEPASLGOASIQNGKDTAPQRYVA 513
DB 421 ASPPLGLEERKKTPTPTSTNSVLSTNRSNPSLLEPASLGOASIQNGKDTAPQRYVA 480
QY 514 SPBAHNISSSGGA PDRTPNPRGVSSRSTFHAGQLROVRDQONLPYGVTPASPSGHSQGR 573
DB 481 SPBAHNISSSGGA PDRTPNPRGVSSRSTFHAGQLROVRDQONLPYGVTPASPSGHSQGR 540
QY 574 GAGSIFSKFTSKFVRNLLNEPESKQVETLRPHVVGSGNDKEKEFRFAKPRSLRFTW 633
DB 541 GAGSIFSKFTSKFVRNLLNEPESKQVETLRPHVVGSGNDKEKEFRFAKPRSLRFTW 600
QY 634 SMKTTSSMEPNEMREIRKYLVDANSQSELEHEKYMILCMHGTGHEDFVQEMEVCKLPR 693
DB 601 SMKTTSSMEPNEMREIRKYLVDANSQSELEHEKYMILCMHGTGHEDFVQEMEVCKLPR 660
QY 694 LSLNGVRFKRIISGTSMAFKNIASKIANELKL 724
DB 661 LSLNGVRFKRIISGTSMAFKNIASKIANELKL 691

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OM protein - protein search, using sw model

Run on: February 26, 2005, 17:43:07 ; Search time 43 Seconds
(without alignments)
1256.882 Million cell updates/sec

Title: US-10-760-407-2

Perfect score: 3737

Sequence: 1 MSARPTPLTNRDTEQPT.....SGTSMAPKTIASKIANKL 724

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodaca/1/1aa/5A COMB.pep.*
 - 2: /cgn2_6/ptodaca/1/1aa/5B COMB.pep.*
 - 3: /cgn2_6/ptodaca/1/1aa/6A COMB.pep.*
 - 4: /cgn2_6/ptodaca/1/1aa/6B COMB.pep.*
 - 5: /cgn2_6/ptodaca/1/1aa/PTUS COMB.pep.*
 - 6: /cgn2_6/ptodaca/1/1aa/backfilea1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3737	100.0	724	4 US-09-984-890-2	Sequence 2, App11
2	3737	100.0	724	4 US-10-274-194-2	Sequence 2, App11
3	3654	97.8	722	4 US-09-984-890-4	Sequence 4, App11
4	3654	97.8	722	4 US-10-274-194-4	Sequence 4, App11
5	3644	97.5	722	4 US-08-817-832B-32	Sequence 32, App1
6	3566	95.4	691	4 US-09-949-016-8255	Sequence 8255, App
7	3566	95.4	691	4 US-09-949-016-8256	Sequence 8256, App
8	3515	94.1	745	4 US-09-523-849-36	Sequence 36, App1
9	2555	68.4	793	4 US-09-523-849-32	Sequence 32, App1
10	2513	67.2	602	4 US-09-949-016-7417	Sequence 7417, App
11	2513	67.2	602	4 US-09-949-016-7418	Sequence 7418, App
12	2464	65.9	729	4 US-08-817-832B-31	Sequence 31, App1
13	2399	64.2	729	2 US-08-677-298-2	Sequence 2, App11
14	2399	64.2	729	4 US-09-523-849-33	Sequence 33, App1
15	2399	64.2	724	4 US-09-949-016-8234	Sequence 8234, App
16	2381	63.7	713	4 US-09-538-092-1022	Sequence 1022, App
17	2381	63.7	713	4 US-09-949-016-6214	Sequence 6214, App
18	1130.5	30.3	604	4 US-09-523-849-35	Sequence 35, App1
19	1016	27.2	776	4 US-09-523-849-34	Sequence 34, App1
20	986	26.4	776	4 US-10-116-326-2	Sequence 2, App11
21	827	22.1	778	4 US-08-357-806C-43	Sequence 43, App1
22	827	22.1	778	4 US-09-538-092-212	Sequence 212, App
23	797.5	21.3	633	4 US-09-633-328B-3	Sequence 3, App11
24	797.5	21.3	633	4 US-09-824-735-3	Sequence 2, App11
25	797.5	21.3	668	4 US-09-930-181-2	Sequence 2, App11
26	797.5	21.3			
27	793.5	21.2			

28	757.5	20.3	512	4 US-09-633-328B-2	Sequence 2, App11
29	756.5	20.2	418	4 US-09-248-796A-18441	Sequence 18441, A
30	727.5	19.5	511	4 US-09-633-328B-4	Sequence 4, App11
31	711	19.0	703	4 US-10-116-326-6	Sequence 6, App11
32	710	19.0	557	4 US-09-949-016-10174	Sequence 10174, A
33	709	19.0	552	4 US-09-824-735-4	Sequence 4, App11
34	708	18.9	552	4 US-09-538-092-1212	Sequence 1212, App
35	705.5	18.9	552	4 US-08-557-806C-40	Sequence 40, App1
36	698	18.7	504	4 US-09-554-726A-10	Sequence 10, App1
37	694	18.6	257	2 US-07-857-824B-25	Sequence 25, App1
38	690.5	18.5	345	3 US-09-101-146-1	Sequence 1, App11
39	681	18.2	1064	4 US-09-538-092-154	Sequence 154, App
40	680	18.2	631	4 US-09-579-664B-11	Sequence 11, App1
41	680	18.2	631	4 US-10-355-975A-11	Sequence 11, App1
42	677	18.1	504	4 US-09-554-726A-14	Sequence 14, App1
43	675.5	18.1	630	4 US-10-355-975A-38	Sequence 38, App1
44	667	17.8	436	4 US-09-734-673-2	Sequence 2, App11
45	667	17.8	436	4 US-09-523-849-2	Sequence 2, App11

ALIGNMENTS

RESULT 1									
US-09-984-890-2									
Sequence 2, Application US/09984890									
Patent No. 6492156									
GENERAL INFORMATION:									
APPLICANT: YAN, Chunhua et al.									
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC									
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES									
FILE REFERENCE: CL001306									
CURRENT APPLICATION NUMBER: US/09/984,890									
CURRENT FILING DATE: 2001-10-31									
NUMBER OF SEQ ID NOS: 4									
SOFTWARE: FastSeq for Windows Version 4.0									
SEQ ID NO 2									
LENGTH: 724									
TYPE: PRT									
ORGANISM: Homo sapiens									
US-09-984-890-2									
Query Match									
Best Local Similarity 100.0%; Score 3737; DB 4; Length 724;									
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MSARPTPLTNRDTEQPTLGHLDSPKSKNMIRGNSATSDAEQPHIGNTRRLKTTG	60						
DB	1	MSARPTPLTNRDTEQPTLGHLDSPKSKNMIRGNSATSDAEQPHIGNTRRLKTTG	60						
QY	61	KGNFAVKLARHILLTGKEVAVKIIDKTQUNSSLOQLFREVRIMKVLNHNIVKLFVIE	120						
DB	61	KGNFAVKLARHILLTGKEVAVKIIDKTQUNSSLOQLFREVRIMKVLNHNIVKLFVIE	120						
QY	121	TEKTLVLNVEYASGSEVFYLVVHGMKEKEAAKROVTSVAYQYCHQKTYVHBDLKAEN	180						
DB	121	TEKTLVLNVEYASGSEVFYLVVHGMKEKEAAKROVTSVAYQYCHQKTYVHBDLKAEN	180						
QY	181	LILDAAMNLIKADFGSNEFTFGNKLDTFCGSPYVAPLFOGKKYDGPVDVMSLGVIL	240						
DB	181	LILDAAMNLIKADFGSNEFTFGNKLDTFCGSPYVAPLFOGKKYDGPVDVMSLGVIL	240						
QY	241	YTLVSGSLPDPGQNLKELRERVLGKRYRIPFYVSTDCENLLKKFLILNPSKGTLEQIMK	300						
DB	241	YTLVSGSLPDPGQNLKELRERVLGKRYRIPFYVSTDCENLLKKFLILNPSKGTLEQIMK	300						
QY	301	DRMANTGHEDDELKPYVEPLPDYKDRRRTLAMSQYTRREIDSLVGQYVNEVMAITYLL	360						
DB	301	DRMANTGHEDDELKPYVEPLPDYKDRRRTLAMSQYTRREIDSLVGQYVNEVMAITYLL	360						
QY	361	LGYKSELEDDTTLTKPRPSADLTNSSAPSPSHKQVRSVSNPKORRFSQQAIPATPSN	420						
DB	361	LGYKSELEDDTTLTKPRPSADLTNSSAPSPSHKQVRSVSNPKORRFSQQAIPATPSN	420						

Db 361 LGYKSELEBDDITTLKPRPSADLTNNSAPSPSHKQVSANPKORRPSDQGPALPTSN 420
Qy 421 SYSKKTQSNNAENKRPREDRESGRKASSTAKVPASPLPGLERKTTPTPTSTNSVLSTSTN 480
Db 421 SYSKKTQSNNAENKRPREDRESGRKASSTAKVPASPLPGLERKTTPTPTSTNSVLSTSTN 480
Qy 481 RSRNSPLERASLQASLQNGKDSAPQRPVPAASPAHNISSSGAPDRTNPPRGVSSRS 540
Db 481 RSRNSPLERASLQASLQNGKDSAPQRPVPAASPAHNISSSGAPDRTNPPRGVSSRS 540
Qy 541 TFHAGQLRQVDDQNLPGVTPPASPSGHSQGRGASGSIFSFTSKFVRRLNLEPESKDR 600
Db 541 TFHAGQLRQVDDQNLPGVTPPASPSGHSQGRGASGSIFSFTSKFVRRLNLEPESKDR 600
Qy 601 VETLRPHVVGSGGNDKEKEEFREAKPRSLRFTWSMKTTSMEPNMREIRKVLANDNSCQ 660
Db 601 VETLRPHVVGSGGNDKEKEEFREAKPRSLRFTWSMKTTSMEPNMREIRKVLANDNSCQ 660
Qy 661 SELHEKYMMLCMHGTGPHEDFVQWEMEVCKLPRLSLNGVRPKRISGTSMAFKNIASKIAN 720
Db 661 SELHEKYMMLCMHGTGPHEDFVQWEMEVCKLPRLSLNGVRPKRISGTSMAFKNIASKIAN 720
Qy 721 ELKL 724
Db 721 ELKL 724

RESULT 2

US-10-274-194-2
Sequence 2, Application US/10274194
Patent No. 6706511
GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: CL001306DIV
CURRENT APPLICATION NUMBER: US/10/274,194
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 724
TYPE: PRT
ORGANISM: Homo sapiens
US-10-274-194-2

Query Match 100.0%; Score 3737; DB 4; Length 724;
Best Local Similarity 100.0%; Pred. No. 5.3e-272;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSSARTPLPTLNERTDTEOPTLGHLDSPSSKSNMIRGNASATSADOPHIGNYRLTKTIG 60
Db 1 MSSARTPLPTLNERTDTEOPTLGHLDSPSSKSNMIRGNASATSADOPHIGNYRLTKTIG 60
Qy 61 KGNFAKVLARHILITGKEVAVAKIIDKTQNLSSSIQKLFREVRIMKVLNHPNIVLFEVIE 120
Db 61 KGNFAKVLARHILITGKEVAVAKIIDKTQNLSSSIQKLFREVRIMKVLNHPNIVLFEVIE 120
Qy 121 TEKTLIYLMVEYASGGEVFDYLVAHGRMKEKARAKRQVAVOYCHQKFIYHRDLKAEN 180
Db 121 TEKTLIYLMVEYASGGEVFDYLVAHGRMKEKARAKRQVAVOYCHQKFIYHRDLKAEN 180
Qy 181 LLLDADNMKIKIADFGSNEFTFGNKLDTFCGSPPYAPAPLFOGKKYGDGEVDWVMSLGVTL 240
Db 181 LLLDADNMKIKIADFGSNEFTFGNKLDTFCGSPPYAPAPLFOGKKYGDGEVDWVMSLGVTL 240
Qy 241 YTLVSGSLPFDGQNLKELREVRILRGKYRIPTYMSTDCENILKKFLILNPSKRGTLQIMK 300
Db 241 YTLVSGSLPFDGQNLKELREVRILRGKYRIPTYMSTDCENILKKFLILNPSKRGTLQIMK 300
Qy 301 DMMNVVGHEDDLKPYVEPLPYKDPRRRTLMVSMGYTBEIQDSIVGQRINVEWATYLL 360
Db 301 DMMNVVGHEDDLKPYVEPLPYKDPRRRTLMVSMGYTBEIQDSIVGQRINVEWATYLL 360

Db 301 DMMNVVGHEDDLKPYVEPLPYKDPRRRTLMVSMGYTBEIQDSIVGQRINVEWATYLL 360
Qy 361 LGYKSELEBDDITTLKPRPSADLTNNSAPSPSHKQVSANPKORRPSDQGPALPTSN 420
Db 361 LGYKSELEBDDITTLKPRPSADLTNNSAPSPSHKQVSANPKORRPSDQGPALPTSN 420
Qy 421 SYSKKTQSNNAENKRPREDRESGRKASSTAKVPASPLPGLERKTTPTPTSTNSVLSTSTN 480
Db 421 SYSKKTQSNNAENKRPREDRESGRKASSTAKVPASPLPGLERKTTPTPTSTNSVLSTSTN 480
Qy 481 RSRNSPLERASLQASLQNGKDSAPQRPVPAASPAHNISSSGAPDRTNPPRGVSSRS 540
Db 481 RSRNSPLERASLQASLQNGKDSAPQRPVPAASPAHNISSSGAPDRTNPPRGVSSRS 540
Qy 541 TFHAGQLRQVDDQNLPGVTPPASPSGHSQGRGASGSIFSFTSKFVRRLNLEPESKDR 600
Db 541 TFHAGQLRQVDDQNLPGVTPPASPSGHSQGRGASGSIFSFTSKFVRRLNLEPESKDR 600
Qy 601 VETLRPHVVGSGGNDKEKEEFREAKPRSLRFTWSMKTTSMEPNMREIRKVLANDNSCQ 660
Db 601 VETLRPHVVGSGGNDKEKEEFREAKPRSLRFTWSMKTTSMEPNMREIRKVLANDNSCQ 660
Qy 661 SELHEKYMMLCMHGTGPHEDFVQWEMEVCKLPRLSLNGVRPKRISGTSMAFKNIASKIAN 720
Db 661 SELHEKYMMLCMHGTGPHEDFVQWEMEVCKLPRLSLNGVRPKRISGTSMAFKNIASKIAN 720
Qy 721 ELKL 724
Db 721 ELKL 724

RESULT 3

US-09-984-890-4
Sequence 4, Application US/09984890
Patent No. 6492156
GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: CL001306
CURRENT APPLICATION NUMBER: US/09/984,890
CURRENT FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 722
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-984-890-4

Query Match 97.8%; Score 3654; DB 4; Length 722;
Best Local Similarity 97.8%; Pred. No. 8.9e-266;
Matches 708; Conservative 9; Mismatches 5; Indels 2; Gaps 1;

Qy 1 MSSARTPLPTLNERTDTEOPTLGHLDSPSSKSNMIRGNASATSADOPHIGNYRLTKTIG 60
Db 1 MSSARTPLPTLNERTDTEOPTLGHLDSPSSKSNMIRGNASATSADOPHIGNYRLTKTIG 60
Qy 61 KGNFAKVLARHILITGKEVAVAKIIDKTQNLSSSIQKLFREVRIMKVLNHPNIVLFEVIE 120
Db 61 KGNFAKVLARHILITGKEVAVAKIIDKTQNLSSSIQKLFREVRIMKVLNHPNIVLFEVIE 120
Qy 121 TEKTLIYLMVEYASGGEVFDYLVAHGRMKEKARAKRQVAVOYCHQKFIYHRDLKAEN 180
Db 121 TEKTLIYLMVEYASGGEVFDYLVAHGRMKEKARAKRQVAVOYCHQKFIYHRDLKAEN 180
Qy 181 LLLDADNMKIKIADFGSNEFTFGNKLDTFCGSPPYAPAPLFOGKKYGDGEVDWVMSLGVTL 240
Db 181 LLLDADNMKIKIADFGSNEFTFGNKLDTFCGSPPYAPAPLFOGKKYGDGEVDWVMSLGVTL 240
Qy 241 YTLVSGSLPFDGQNLKELREVRILRGKYRIPTYMSTDCENILKKFLILNPSKRGTLQIMK 300
Db 241 YTLVSGSLPFDGQNLKELREVRILRGKYRIPTYMSTDCENILKKFLILNPSKRGTLQIMK 300

Db 241 YTVVSGSLPPDQGNLKELRERVLGRKYRIPFYMSTDCENLLKFFLIINPSKRGTLLEQIMK 300
Qy 301 DRMMNVGHEDDELKPYVEPLPDYKDPRTTELMMVSMGTTRREIQLSLVGQRNEVMATYLL 360
Db 301 DRMMNVGHEDDELKPYVEPLPDYKDPRTTELMMVSMGTTRREIQLSLVGQRNEVMATYLL 360
Qy 361 LGYSSSELEBDITTLKRPSPADLTNNSAPSPSHKVQSVANPKQRFPSDQAGPAITSN 420
Db 361 LGYSSSELEBDITTLKRPSPADLTNNSAPSPSHKVQSVANPKQRFPSDQAGPAITSN 420
Qy 421 SYSKKTOSNNAENKRRPEEDRESGRKASTAKVPASPLPGLERKKTTPPTSTNSVLSSTN 480
Db 421 SYSKKTOSNNAENKRRPEE - ETGRKASTAKVPASPLPGLDRKKTTPPTSTNSVLSSTN 478
Qy 481 RSRNSPLLEBASLGQASIQNGKDSAPQRPVSPSAHNISSSGADRTNPPRGVSRS 540
Db 479 RSRNSPLLEBASLGQASIQNGKDSAPQRPVSPSAHNISSSGADRTNPPRGVSRS 538
Qy 541 TFFAGOLROYRDQONLPYGTVPASPSGHSQGRGASGIFSKFTSKFVRRLNBPESKDR 600
Db 539 TFFAGOLROYRDQONLPFGVTPASPSGHSQGRGASGIFSKFTSKFVRRLNBPESKDR 598
Qy 601 VETLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPEMMREIRKVLDA NSCQ 660
Db 599 VETLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPEMMREIRKVLDA NSCQ 658
Qy 661 SELHEKTMILCMGTPGHEDFVQWEMEVCKLPRLSLNGVRFKRISGTSMAFKNIASKIAN 720
Db 659 SELHERYMLLCVHGTPGHENFVQWEMEVCKLPRLSLNGVRFKRISGTSMAFKNIASKIAN 718
Qy 721 ELKL 724
Db 719 ELKL 722

RESULT 4
US-10-274-194-4
; Sequence 4, Application US/10274194
; Patent No. 6706511
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO01306DIV
; CURRENT APPLICATION NUMBER: US/10/274,194
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 722
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-274-194-4

Query Match 97.8%; Score 3654; DB 4; Length 722;
Best Local Similarity 97.8%; Pred. No. 8.9e-26;
Matches 708; Conservative 9; Mismatches 5; Indels 2; Gaps 1;
Qy 1 MSARTEPLTNERDEQPTLGHLDSPSSKSNMIRGRNSATSADQPHIGNRLTKTIG 60
Db 1 MSARTEPLTNERDEQPTLGHLDSPSSKSNMIRGRNSATSADQPHIGNRLTKTIG 60
Qy 61 KGNPAKVKLARHILTGKEVAVKIIDKTQLNSSSIQKLFREVRIKVLNHNIVLFEVIE 120
Db 61 KGNPAKVKLARHILTGKEVAVKIIDKTQLNSSSIQKLFREVRIKVLNHNIVLFEVIE 120
Qy 121 TEKTLVYMEYASGGEYFDVLVAHGRMKEKARAKKFOVYSAVOYCHQKTIYHDLKAEN 180
Db 121 TEKTLVYMEYASGGEYFDVLVAHGRMKEKARAKKFOVYSAVOYCHQKTIYHDLKAEN 180
Qy 181 LLLDADNNIKIADGFGNEFTFGNKLDTPFGSGPPYAPBELFOGKKYDGPEDVWVSLGVL 240

Db 181 LLLDADNNIKIADGFGNEFTFGNKLDTPFGSGPPYAPBELFOGKKYDGPEDVWVSLGVL 240
Qy 241 YTVVSGSLPPDQGNLKELRERVLGRKYRIPFYMSTDCENLLKFFLIINPSKRGTLLEQIMK 300
Db 241 YTVVSGSLPPDQGNLKELRERVLGRKYRIPFYMSTDCENLLKFFLIINPSKRGTLLEQIMK 300
Qy 301 DRMMNVGHEDDELKPYVEPLPDYKDPRTTELMMVSMGTTRREIQLSLVGQRNEVMATYLL 360
Db 301 DRMMNVGHEDDELKPYVEPLPDYKDPRTTELMMVSMGTTRREIQLSLVGQRNEVMATYLL 360
Qy 361 LGYSSSELEBDITTLKRPSPADLTNNSAPSPSHKVQSVANPKQRFPSDQAGPAITSN 420
Db 361 LGYSSSELEBDITTLKRPSPADLTNNSAPSPSHKVQSVANPKQRFPSDQAGPAITSN 420
Qy 421 SYSKKTOSNNAENKRRPEEDRESGRKASTAKVPASPLPGLERKKTTPPTSTNSVLSSTN 480
Db 421 SYSKKTOSNNAENKRRPEE - ETGRKASTAKVPASPLPGLDRKKTTPPTSTNSVLSSTN 478
Qy 481 RSRNSPLLEBASLGQASIQNGKDSAPQRPVSPSAHNISSSGADRTNPPRGVSRS 540
Db 479 RSRNSPLLEBASLGQASIQNGKDSAPQRPVSPSAHNISSSGADRTNPPRGVSRS 538
Qy 541 TFFAGOLROYRDQONLPYGTVPASPSGHSQGRGASGIFSKFTSKFVRRLNBPESKDR 600
Db 539 TFFAGOLROYRDQONLPFGVTPASPSGHSQGRGASGIFSKFTSKFVRRLNBPESKDR 598
Qy 601 VETLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPEMMREIRKVLDA NSCQ 660
Db 599 VETLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPEMMREIRKVLDA NSCQ 658
Qy 661 SELHEKTMILCMGTPGHEDFVQWEMEVCKLPRLSLNGVRFKRISGTSMAFKNIASKIAN 720
Db 659 SELHERYMLLCVHGTPGHENFVQWEMEVCKLPRLSLNGVRFKRISGTSMAFKNIASKIAN 718
Qy 721 ELKL 724
Db 719 ELKL 722

RESULT 5
US-08-817-832B-32
; Sequence 32, Application US/08817832B
; Patent No. 6579691
; GENERAL INFORMATION:
; APPLICANT: MANDELKOW, Eckhard, et al.
; TITLE OF INVENTION: No. 6579691el Protein Kinase (NPK-110)
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 S. Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: US
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,832B
; FILING DATE: 28-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/04258
; FILING DATE: 30-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94 11 7122.5
; FILING DATE: 28-OCT-1994
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 722 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-817-832B-32

Query Match 97.5%; Score 3644; DB 4; Length 722;
Best Local Similarity 97.5%; Pred. No. 5e-265;
Matches 706; Conservative 9; Mismatches 7; Indels 2; Gaps 1;

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QY 1 MSSARTPLPTLNRPDTPHGLHLDSPSSKSNMIRGNSATSDADOPHIGNRLKTTIG 60
DB 1 MSSARTPLPTLNRPDTPHGLHLDSPSSKSNMIRGNSATSDADOPHIGNRLKTTIG 60
QY 61 KGNFAKYKLARHILITGKEVAVKIIDKTQLNSSSLQKLFREVRIMKYLHNHYKLFVIE 120
DB 61 KGNFAKYKLARHILITGKEVAVKIIDKTQLNSSSLQKLFREVRIMKYLHNHYKLFVIE 120
QY 121 TEKTYLVMEYASGGEFVDYVAHGRMKEKARQVAVOYCHOKETIYHRDLKAEN 180
DB 121 TEKTYLVMEYASGGEFVDYVAHGRMKEKARQVAVOYCHOKETIYHRDLKAEN 180
QY 181 LILDADMNITKIADPGSFNEFTGNKLDTPGSGPPYAPBELFOGKTYDGPEDVWMSLGVL 240
DB 181 LILDADMNITKIADPGSFNEFTGNKLDTPGSGPPYAPBELFOGKTYDGPEDVWMSLGVL 240
QY 241 YTVSGSLPFDGQNLKELRERVLRGKYRIPFYMSDTCENLLKKFLILNPSKGTLEQIMK 300
DB 241 YTVSGSLPFDGQNLKELRERVLRGKYRIPFYMSDTCENLLKKFLILNPSKGTLEQIMK 300
QY 301 DRMNANGHEDELKPYVEPLPDYKDPRTTELAMVSMGYTRREIODSLVGQRVNEVMAITYLL 360
DB 301 DRMNANGHEDELKPYVEPLPDYKDPRTTELAMVSMGYTRREIODSLVGQRVNEVMAITYLL 360
QY 361 LGYKSELEEDTTLTKPRPSADLTNSAPSPSHKQSVSANPKORRSPDQAPALPTSN 420
DB 361 LGYKSELEEDTTLTKPRPSADLTNSAPSPSHKQSVSANPKORRSPDQAPALPTSN 420
QY 421 SYKTKQSNNAENKREEDRESGRKASTAKVPASPLPGLERKKTPTPESTNSVLTSTN 480
DB 421 SYKTKQSNNAENKREEDRESGRKASTAKVPASPLPGLERKKTPTPESTNSVLTSTN 480
QY 481 RSNSPLLEBASIGQASIONGKOSTAPORVPVAPSAHNISSSGAPDRTNPRGVSSRS 540
DB 481 RSNSPLLEBASIGQASIONGKOSTAPORVPVAPSAHNISSSGAPDRTNPRGVSSRS 540
QY 541 TFHAGQLROVRDQONLPYGVPASPSPGSHQGRGSGSIFSKTSPFVRNINLEPESKOR 600
DB 541 TFHAGQLROVRDQONLPYGVPASPSPGSHQGRGSGSIFSKTSPFVRNINLEPESKOR 600
QY 601 VETLRPHVVGSGNDKEKEFEAKPRSLRFTWSMKTTSSMEPNEMMRERIKVLDANSCQ 660
DB 601 VETLRPHVVGSGNDKEKEFEAKPRSLRFTWSMKTTSSMEPNEMMRERIKVLDANSCQ 660
QY 661 SEIHEKYMILCMHGTGHEDFVQWEMEVCKLPRLSLNGVRFKRIISGTSMAFKNIASKIAN 720
DB 661 SEIHEKYMILCMHGTGHEDFVQWEMEVCKLPRLSLNGVRFKRIISGTSMAFKNIASKIAN 720
QY 721 ELKL 724
DB 719 ELKL 722
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RESULT 6
US-09-949-016-8255
Sequence 8255 Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8255
LENGTH: 691
TYPE: PRT
ORGANISM: Human
US-09-949-016-8255

Query Match 95.4%; Score 3566; DB 4; Length 691;
Best Local Similarity 99.9%; Pred. No. 3.4e-259;
Matches 690; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 34 MIRGNSATSADOPHIGNRYRLKTTIGKGNFAKYKLARHILITGKEVAVKIIDKTQLNSSS 93
DB 1 MIRGNSATSADOPHIGNRYRLKTTIGKGNFAKYKLARHILITGKEVAVKIIDKTQLNSSS 93
QY 94 LQKLFREVRIMKYLHNHYKLFVIEETKTYLVMEYASGGEFVDYVAHGRMKEKAR 153
DB 61 LQKLFREVRIMKYLHNHYKLFVIEETKTYLVMEYASGGEFVDYVAHGRMKEKAR 120
QY 154 AKFROVSAVOYCHOKETIYHRDLKAENLILDADMNITKIADPGSFNEFTGNKLDTPGSGP 213
DB 121 AKFROVSAVOYCHOKETIYHRDLKAENLILDADMNITKIADPGSFNEFTGNKLDTPGSGP 180
QY 214 PYAABELFOGKTYDGPEDVWMSLGVLITVLSGSLPFDQNLKELRERVLRGKYRIPFYM 273
DB 181 PYAABELFOGKTYDGPEDVWMSLGVLITVLSGSLPFDQNLKELRERVLRGKYRIPFYM 240
QY 274 STDCENLKKFLILNPSKGTLEQIMKORMNANGHEDELKPYVEPLPDYKDPRTTELAMV 333
DB 241 STDCENLKKFLILNPSKGTLEQIMKORMNANGHEDELKPYVEPLPDYKDPRTTELAMV 300
QY 334 SMGYTRREIODSLVGQRVNEVMAITYLLGYKSELEEDTTLTKPRPSADLTNSAPSPSH 393
DB 301 SMGYTRREIODSLVGQRVNEVMAITYLLGYKSELEEDTTLTKPRPSADLTNSAPSPSH 360
QY 394 KYORSVSNPKORRSPDQAPALPTNSNSYSKKTQSNNAENKREEDRESGRASSTAKVP 453
DB 361 KYORSVSNPKORRSPDQAPALPTNSNSYSKKTQSNNAENKREEDRESGRASSTAKVP 420
QY 454 ASPLPGLERKKTPTPESTNSVLTSTNSRNSPLLEBASIGQASIONGKOSTAPORVPA 513
DB 421 ASPLPGLERKKTPTPESTNSVLTSTNSRNSPLLEBASIGQASIONGKOSTAPORVPA 480
QY 514 SPSAHNISSSGAPDRTNPRGVSSRSTPHAGQLROVRDQONLPYGVPASPSPGSHQGR 573
DB 481 SPSAHNISSSGAPDRTNPRGVSSRSTPHAGQLROVRDQONLPYGVPASPSPGSHQGR 540
QY 574 GASGSIKSKTSPFVRNINLEPESKORVETLRPHVVGSGNDKEKEFEAKPRSLRFTW 633
DB 541 GASGSIKSKTSPFVRNINLEPESKORVETLRPHVVGSGNDKEKEFEAKPRSLRFTW 600
QY 634 SMKTTSSMEPNEMMRERIKVLDANSCOSEIHEKYMILCMHGTGHEDFVQWEMEVCKLP 693
DB 601 SMKTTSSMEPNEMMRERIKVLDANSCOSEIHEKYMILCMHGTGHEDFVQWEMEVCKLP 660
QY 694 LSLNGVRFKRIISGTSMAFKNIASKIANELKL 724
DB 661 LSLNGVRFKRIISGTSMAFKNIASKIANELKL 691
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RESULT 7
US-09-949-016-8256
Sequence 8256 Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

```
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: C1001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/223,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 8256
/ LENGTH: 691
/ TYPE: PR1
/ ORGANISM: Human
US-09-949-016-8256
```

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Query Match          95.4%; Score 3566; DB 4; Length 691,
Best Local Similarity 99.9%; Pred. No. 3,4e-259;
Matches 690; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 34 MINGRNSATSADQPHIGNYRLKTIKGNFAVKLARHILITGEVAVKIIDKTQLNSS 93
DB 1 MINGRNSATSADQPHIGNYRLKTIKGNFAVKLARHILITGEVAVKIIDKTQLNSS 60
QY 94 LQKLFREVRIMKVLNHNIVKLFVIEETKTYLWMEYASGGEVFDYLVHGRMKEAR 153
DB 61 LQKLFREVRIMKVLNHNIVKLFVIEETKTYLWMEYASGGEVFDYLVHGRMKEAR 120
QY 154 AKFROVSAVOYCHQKFIYHRDLKAENLLDADNMIKIADFGSNEFTFGNKIDTFGSP 213
DB 121 AKFROVSAVOYCHQKFIYHRDLKAENLLDADNMIKIADFGSNEFTFGNKIDTFGSP 180
QY 214 PYAAPBELFOGKKYDGEVDWWSLGVILYTVSSGLPFDGQNLKELRERVLRGKRIIPFM 273
DB 181 PYAAPBELFOGKKYDGEVDWWSLGVILYTVSSGLPFDGQNLKELRERVLRGKRIIPFM 240
QY 274 STDCENLLKKFLLINPSKRGTLBOIMKDRMNVGHEDDELKPYVEPLPDYKDPRTTLMV 333
DB 241 STDCENLLKKFLLINPSKRGTLBOIMKDRMNVGHEDDELKPYVEPLPDYKDPRTTLMV 300
QY 334 SMGYTREIIDSIVGQRYNEVMATYLLGYKSELEBDITTLKPRPADLTNSAPSPSH 393
DB 301 SMGYTREIIDSIVGQRYNEVMATYLLGYKSELEBDITTLKPRPADLTNSAPSPSH 360
QY 394 KVOBSVSNPKORRFSQAGPAIPTNSYSKKTQSNNAENKRPEDRESGRKASTAKVP 453
DB 361 KVOBSVSNPKORRFSQAGPAIPTNSYSKKTQSNNAENKRPEDRESGRKASTAKVP 420
QY 454 ASPLPGLERKKTTPPTSTNSVLSTSTNRKNSPLLEBASIGQASIQNGKOSTAPQRPVA 513
DB 421 ASPLPGLERKKTTPPTSTNSVLSTSTNRKNSPLLEBASIGQASIQNGKOSTAPQRPVA 480
QY 514 SPSPAHNISSSGGAPDRNPPRGVSSRSTPHAGOLROVRDOONLPYGVTPASPSSGSGRR 573
DB 481 SPSPAHNISSSGGAPDRNPPRGVSSRSTPHAGOLROVRDOONLPYGVTPASPSSGSGRR 540
QY 574 GASGSIFSFKFTSKFVRNLNEPESKDREVTLRPHVVGSGNDKEKEEFREAKPRSLRFTM 633
DB 541 GASGSIFSFKFTSKFVRNLNEPESKDREVTLRPHVVGSGNDKEKEEFREAKPRSLRFTM 600
QY 634 SMKTTSSMEBENEMREIRKYLNDANSQSELEHEKMYLCHGTFCHHEFPVOMEWCVCLPR 693
DB 601 SMKTTSSMEBENEMREIRKYLNDANSQSELEHEKMYLCHGTFCHHEFPVOMEWCVCLPR 660
QY 694 LSLNGVFRKRIISGTSMAFKNIASKIANEKL 724
DB 661 LSLNGVFRKRIISGTSMAFKNIASKIANEKL 691
```

```
/ Sequence 36, Application US/09523849
/ Patent No. 6458561
/ GENERAL INFORMATION:
/ APPLICANT: Bandman, Olga
/ APPLICANT: Moitenl, Angela
/ APPLICANT: Magnaghi, Paola
/ APPLICANT: Bosotti, Roberta
/ APPLICANT: Scacchi, Emanuela
/ APPLICANT: Isacchi, Antonella
/ APPLICANT: Hodgson, Dave
/ TITLE OF INVENTION: HUMAN NIMI KINASE
/ FILE REFERENCE: PC-0009 US
/ CURRENT APPLICATION NUMBER: US/09/523,849
/ CURRENT FILING DATE: 2000-03-13
/ NUMBER OF SEQ ID NOS: 39
/ SOFTWARE: PERL Program
/ SEQ ID NO 36
/ LENGTH: 745
/ TYPE: PR1
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ OTHER INFORMATION: Genbank Accession No. 6458561 g1749794
US-09-523-849-36
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Query Match          94.1%; Score 3515; DB 4; Length 745,
Best Local Similarity 92.3%; Pred. No. 2,5e-255;
Matches 688; Conservative 1; Mismatches 2; Indels 54; Gaps 1;
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QY 34 MINGRNSATSADQPHIGNYRLKTIKGNFAVKLARHILITGEVAVKIIDKTQLNSS 93
DB 1 MINGRNSATSADQPHIGNYRLKTIKGNFAVKLARHILITGEVAVKIIDKTQLNSS 60
QY 94 LQKLFREVRIMKVLNHNIVKLFVIEETKTYLWMEYASGGEVFDYLVHGRMKEAR 153
DB 61 LQKLFREVRIMKVLNHNIVKLFVIEETKTYLWMEYASGGEVFDYLVHGRMKEAR 120
QY 154 AKFROVSAVOYCHQKFIYHRDLKAENLLDADNMIKIADFGSNEFTFGNKIDTFGSP 213
DB 121 AKFROVSAVOYCHQKFIYHRDLKAENLLDADNMIKIADFGSNEFTFGNKIDTFGSP 180
QY 214 PYAAPBELFOGKKYDGEVDWWSLGVILYTVSSGLPFDGQNLKELRERVLRGKRIIPFM 273
DB 181 PYAAPBELFOGKKYDGEVDWWSLGVILYTVSSGLPFDGQNLKELRERVLRGKRIIPFM 240
QY 274 STDCENLLKKFLLINPSKRGTLBOIMKDRMNVGHEDDELKPYVEPLPDYKDPRTTLMV 333
DB 241 STDCENLLKKFLLINPSKRGTLBOIMKDRMNVGHEDDELKPYVEPLPDYKDPRTTLMV 300
QY 334 SMGYTREIIDSIVGQRYNEVMATYLLGYKSELEBDITTLKPRPADLTNSAPSPSH 393
DB 301 SMGYTREIIDSIVGQRYNEVMATYLLGYKSELEBDITTLKPRPADLTNSAPSPSH 360
QY 394 KVOBSVSNPKORRFSQAGPAIPTNSYSKKTQSNNAENKRPEDRESGRKASTAKVP 453
DB 361 KVOBSVSNPKORRFSQAGPAIPTNSYSKKTQSNNAENKRPEDRESGRKASTAKVP 420
QY 454 ASPLPGLERKKTTPPTSTNSVLSTSTNRKNSPLLEBASIGQASIQNGKOSTLMPGSRAS 503
DB 421 ASPLPGLERKKTTPPTSTNSVLSTSTNRKNSPLLEBASIGQASIQNGKOSTLMPGSRAS 480
QY 504 -----STAPQRPVAPSPAHN 519
DB 481 TASASAASAPDRQHQKMSASVHBNKASGLPPTESNCEVPAPSTAPQRPVAPSPAHN 540
QY 520 ISSSGGAPDRTPNPPRGVSSRSTPHAGOLROVRDOONLPYGVTPASPSSGSGRRGASGSI 579
DB 541 ISSSGGAPDRTPNPPRGVSSRSTPHAGOLROVRDOONLPYGVTPASPSSGSGRRGASGSI 600
QY 580 FSKFTSKFVRNLNEPESKDREVTLRPHVVGSGNDKEKEEFREAKPRSLRFTSMKTTSS 639
DB 601 FSKFTSKFVRNLNEPESKDREVTLRPHVVGSGNDKEKEEFREAKPRSLRFTSMKTTSS 660
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QY      640 SMEPMEMREIRKVLVDANSQSELEHEKMYL:CMHSTPGHEDFVQWEMEVCKLPRLSLNGV 699
DB      661 SMEPMEMREIRKVLVDANSQSELEHEKMYL:CMHSTPGHEDFVQWEMEVCKLPRLSLNGV 720
QY      700 RPKRISGTSMAFKNIASKIANELKL 724
DB      721 RPKRISGTSMAFKNIASKIANELKL 745

RESULT 9
US-09-523-849-32
; Sequence 32, Application US/09523849
; Patent No. 6458561
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Molteni, Angela
; APPLICANT: Magnaghi, Paola
; APPLICANT: Bosotti, Roberta
; APPLICANT: Scacchi, Emanuela
; APPLICANT: Isacchi, Antonella
; APPLICANT: Hodgson, Dave
; TITLE OF INVENTION: HUMAN NIM1 KINASE
; FILE REFERENCE: PC-0009 US
; CURRENT APPLICATION NUMBER: US/09/523, 849
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PERL Program
; SEQ ID NO 32
; LENGTH: 793
; TYPE: FRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Genbank Accession No. 6458561 g2052189
US-09-523-849-32

Query Match      68.4%; Score 2555; DB 4; Length 793;
Best Local Similarity 65.5%; Pred. No. 3,1e-183;
Matches 525; Conservative 82; Mismatches 105; Indels 90; Gaps 14;

QY      3 SARPLPTLNERPTDEQTL--GHLD-----SKSSSKSMIRGNSATS-DEQPHIGNR 54
DB      2 SARPLPTLNERPTDEQTLVDTETHPPTKSSSRNIPRCHNSITSATDEQPHIGNYK 61
QY      55 LKLTIGKGNFAKYLAARHILTKGEVAVKIIDKTQUNSSLOKLFREVRIMKVLNHPNIYK 114
DB      62 LKLTIGKGNFAKYLAARHILTKGEVAVKIIDKTQUNSSLOKLFREVRIMKVLNHPNIYK 121
QY      115 LFEVILETEKTYLVMEYASGGEVFDYLVAHGMRKEKARAKFRQVSAVOYCHQKFIYH 174
DB      122 LFEVILETEKTYLVMEYASGGEVFDYLVAHGMRKEKARAKFRQVSAVOYCHQKFIYH 181
QY      175 DLAEENLLDADNMIKADFGSNEFTPGNKLDTPFGSGPPYAPAPLFOGKYDGEVDW 234
DB      182 DLAEENLLDADNMIKADFGSNEFTPGNKLDTPFGSGPPYAPAPLFOGKYDGEVDW 241
QY      235 SLGVIIYTLVSGSLPFDGQNLKELRERVLGKTRIPFYMSIDCENLLKKEFLIINPSKGT 294
DB      242 SLGVIIYTLVSGSLPFDGQNLKELRERVLGKTRIPFYMSIDCENLLKKEFLIINPSKGT 301
QY      295 LEOIMDRMNVNVEHDEDELKPYEPLDYDKDPRTLELVMSQVTRREIODSLVQGRYNEV 354
DB      302 LEOIMDRMNVNVEHDEDELKPYEPELDINDAKRIDIMVTMGFARDINDALVSGKYDEY 361
QY      355 MATYLLIGYKSSLEGG-----DTITLKPRPSADLNNSSAGPSH-KYGRSVSANKQKR 407
DB      362 MATYLLIGYKSPPEEGESLSSGNLCQSRPSSDLNNSTLQSPAHLLKVRSTISANQKQKR 421
QY      408 FSDQAGPAIPTNSYSYKKTQSNNAENKRPDE--DRESGRASST-----AKVPASLPJGLE 461
DB      422 FSDHAGPSIPPAVSYTKRPOANSVESEQKEBMDKDTARLGSTTYGSSSEVYASPLVGED 481
QY      462 RKKTFPTSTNVSILSTYKRSNSPLLEPASLGQASIQNGKDS----- 504

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DB      482 RKKSSAGPS--NNYSGSMTTRNTYVCERSTDRYALQNGRDSLTTEMSSSSTGTYV 540
QY      505 -----PAP-----ORVPASPSANISSGGA 526
DB      541 ASAGPSARPRHOKSMSTSGHPKIVTLPTIKDSEAVRPECTAORVPAASASISAS--T 598
QY      527 PDRTFNPRGVSSRSTFHAGQLRQVRDQNLPGYVTPASPS-----GHSQGRGASGISFEK 582
DB      599 PDRTRPPRGSSSRSTFHGEQL-----RERRSAYSGPSAPSPSHDTAALAHARRGTSIGTISK 655
QY      583 FTSKPYRRLNLPESDRVETLRPHVVGSGNDKEKEFEREAKPRPSLFTWGMKTTSSME 642
DB      656 ITSKEFYRDPSSGEASGRDVTAR---GSSGEPKDEBGEKAKPRSLRFTWGMKTTSSMD 711
QY      643 PNMKREIRKVLVDANSQSELEHEKMYL:CMHSTPGHEDFVQWEMEVCKLPRLSLNGVRFK 702
DB      712 PNDVREIRKVLVDANTCOVEGRERFLPCVHDAQODSLVQWEMEVCKLPRLSLNGVAFK 771
QY      703 RISGTSMAFKNIASKIANELKL 724
DB      772 RISGTSMAFKNIASKIANELKL 793

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RESULT 10
US-09-949-016-7417
; Sequence 7417, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; PRIOR APPLICATION NUMBER: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7417
; LENGTH: 602
; TYPE: FRT
; ORGANISM: Human
US-09-949-016-7417

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Query Match      67.2%; Score 2513; DB 4; Length 602;
Best Local Similarity 88.1%; Pred. No. 3e-180;
Matches 504; Conservative 5; Mismatches 19; Indels 44; Gaps 5;

QY      16 TEQPTLGLDSEKSPSSKSMIRGNSATSADQPHIGNYRLKLTIGKGNFAKYLAARHILT 75
DB      34 SSRPTLGLDSEKSPSSKSMIRGNSATSADQPHIGNYRLKLTIGKGNFAKYLAARHILT 93
QY      76 GKEVAVKIIDKTQUNSSLOKLFREVRIMKVLNHPNIYKLFVETETKTYLVMEYASGG 135
DB      94 GKEVAVKIIDKTQUNSSLOKLFREVRIMKVLNHPNIYKLFVETETKTYLVMEYASGG 153
QY      136 EVFPLYLVAHGMRKEKARAKFRQVSAVOYCHQKFIYHRLKAEENLLDADNMIKADFG 195
DB      154 EVFPLYLVAHGMRKEKARAKFRQVSAVOYCHQKFIYHRLKAEENLLDADNMIKADFG 213
QY      196 FSNFTFGNKLDTPFCGSPPYAAPLFOGKYDGEVDVMSLGVIIYTLVSGSLPFDGQNL 255
DB      214 FSNFTFGNKLDTPFCGSPPYAAPLFOGKYDGEVDVMSLGVIIYTLVSGSLPFDGQNL 273
QY      256 KEIAERVLGKTRIPFYMSIDCENLLKKEFLIINPSKGTLEQIMDRMNVNVEHDEDELK 315
DB      274 KEIAERVLGKTRIPFYMSIDCENLLKKEFLIINPSKGTLEQIMDRMNVNVEHDEDELK 333

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[illegible]

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QY      376 KPRPSADLTNSASSPSSHKVRQSVANPKORFSDQAPALPTSNYSYKKTQSNNAENR      435
DB      394 KPRPSADLTNSASSPSSHKVRQSVANPKORFSDQAPALPTSNYSYKKTQSNNAENR      453
QY      436 PEEDRESGRKASSSTAKVPASPLPGLERKTTPTPTSTNSVLSTSTNRSNPSPLERASLQ      495
DB      454 PEEDRESGRKASSSTAKVPASPLPGLERKTTPTPTSTNSVLSTSTNRSNPSPLERASLQ      513
QY      496 ASIQNGDUS -TAP-QRVVVASPPSA----- -HNSSGCGAPDRN--FP 533
DB      514 ASIQNGKDSLTPMSGRASTASASAVSAAAPROHOKMSASVHPNKASGLPPTESNCEVP      573
QY      534 RGVSSRSSTFHAGQLROYVADQONLPGYVTPASP 565
DB      574 R----- -FRQVPACP 583

RESULT 12
US-08-817-832B-31
; Sequence 31, Application US/08817832B
; Patent No. 6579691
; GENERAL INFORMATION:
; APPLICANT: MANDELKOW, Eckhard, et al.
; TITLE OF INVENTION: No. 6579691e1 Protein Kinase (NPK-110)
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 S. Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: US
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,832B
; FILING DATE: 28-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/04258
; FILING DATE: 30-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94 11 7122.5
; FILING DATE: 28-OCT-1994
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 779 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-817-832B-31

Query Match      65.9%; Score 2464; DB 4; Length 779;
Best Local Similarity 64.6%; Pred. No. 2,1e-176;
Matches 510; Conservative 82; Mismatches 112; Indels 86; Gaps 15;

QY      10 TLNERDTQPTGLH-DSKPSKSNMIRGRNSATSA-DEQPHIGNRYLLKTIKGKFNKV      67
DB      1 TENHSTVDGYETHRIPTKSSSRQNI PRCRSRISATDEQGHIGNRYLQTIKGKFNKV      60
QY      68 KLAHHILITGGEVANKIIDKTQLNSSSIQKLPRFPRIMKVLNHPNIVLFLVETIEKTKLYL      127
DB      61 KLAHHVILTRGEVANKIIDKTQLNPTSLQKLFREVRIMKILNHPNIVLFLVETIEKTKLYL      120
QY      128 VMEVASGGEVVDYLVAHGSMKEKARAKFRQVSAVOYCHQKFTVHRDLKAKENLLDADM      187
DB      121 VMEVASGGEVVDYLVAHGSMKEKARAKFRQVSAVOYCHQKCLVHRDLKAKENLLDADM      180
QY      188 NIKIADFGSNEFTFGKLDITFCGSPPYAAELFQGGKKYDQGEVDVMSGLVILYTLVSGS      247

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Db      181  NIKIADFGFSNEFTGNKLDITFCGSPPYAADELQKKYDPEVDVMSLGIILTVISGS 240
Qy      248  LPFGQNLKEIRER-VLGRKTRIPYMSDCEMLIKFLINPSKGTLEQIMQDMNV 306
Db      241  LPFGQNLKEIRERSCNGKRYVFPYMSDCEMLIKFLINPSKGTLEQIMQDMNV 300
Qy      307  GHEDELKPYVEPLPDYKDPRTTELMSMGYTRIEIDSLVQGHYNEVMAITYLLIGKSS 366
Db      301  GHEBELKPYSEPELDLNDAKRIQIMWTMGARDEINDALVSQKIDEVMATYLLGRKP 360
Qy      367  ELEG-----DTILKPPPSADLTNSSAPSPH-KVQSVANPKORFSDQAPAIPTS 419
Db      361  EFEGGESLSSGNLCQSRPSSDLNNSTLQSPAHKVGRTISANQKQRFSDHAGPSLPPA 420
Qy      420  NSYKKTQSNNAEKRPPE-DRESGRKASSF-----AKVPASPLPGLERKKTPTPTSTNS 473
Db      421  VSYKRPDQANSVEEQKEEMDKDTPARRLGSTTVGSKSEVTASPLVGPDRKSSAGPS-NN 479
Qy      474  VLSTSTSRNSPLERASLGQASIQNGKDS-----504
Db      480  VYSGSGMTRRTTYVCESSTDRYALQNGRDSSTLTEMASMSSTGTVASAGPSARPRQ 539
Qy      505  -----TAP-----ORVPASPSAHNISSGGAPDRTPNPRGVSS 538
Db      540  KSMSTGHPKIVTLPTTKDGEAYRPGTAQRPVAPASPSAHSISAS--TPDRTFPGRSSS 597
Qy      539  RSTHAGQLRVROOQLPYGVTPASPS-----GHSQORAGASGIFSKFTSKVRRRLNE 594
Db      598  RSTHAGQL--RKRSAVSGPPASPSHDTPALAHARRGTSTGILSKITSKVRVRDSE 654
Qy      595  PESKDRVETLRPHVVGSGNDKEKEFEAKPRSLRFTWSMKTSSMEPNEMREIRKYL 654
Db      655  GEASGRIDTAR---GSSGEPKDEKGEAKPR-LRTWSMKTSSMDPDMREIRKYL 709
Qy      655  DANCSELEHEKYMLLCMHGTPGHEDVQWEMEYCKLPLSLNGVRFRKISGTSMAFKNI 714
Db      710  DANCDEOREERFLFCVHDARODSLVQWEMEYCKLPLSLNGVFRKISGTSIAFKNI 769
Qy      715  ASKIANELKL 724
Db      770  ASKIANELKL 779

RESULT 13
US-08-677-298-2
; Sequence 2, Application US/08677298
; Patent No. 5863729
; GENERAL INFORMATION:
; APPLICANT: Plimica-Worms, Helen
; TITLE OF INVENTION: DNA SEQUENCES ENCODING HUMAN TCAR-1
; TITLE OF INVENTION: KINASE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: USA
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,298
; FILING DATE: 09-JUL-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Caruthers, Jennie M.
; REGISTRATION NUMBER: 34,464
; REFERENCE/DOCKET NUMBER: 9-96

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 729 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-677-298-2

Query Match      64.2%; Score 2399; DB 2; Length 729;
Best Local Similarity 66.3%; Pred. No. 1,4e-171;
Matches 503; Conservative 73; Mismatches 115; Indels 68; Gaps 18;

Qy      3  SARTPLPTNERDTPQTLGHLSKPSKSMNIRG-----RNS-ATSADEQPHIGYRLIK 57
Db      2  STRTLPPTVNERDTEHNT-SHGDRQEVTSRFSRGACRNSIASCADEQPHIGYRLIK 60
Qy      58  TTGKGNPAVKLARHILTGKEVAVKIDKTQANSSSLQKLPRVRIMKYLHPNIVKLPFE 117
Db      61  TTGKGNPAVKLARHILTGREVAIKIDKTQANPTSLQKLPRVIMKILHNPVVKLPFE 120
Qy      118  VIETEKTYLVMEVSGSEVFDYLVAGRMKEKEARFQVSVAVQYCHQKFIYHRDLK 177
Db      121  VIETEKTYLVMEVSGSEVFDYLVAGRMKEKEARSFRQIVSAVQYCHQKFIYHRDLK 180
Qy      178  AENLLDADMNKIIDFGPSNEFTGNKLDITFCGSPPYAABELFGKKYDPEVDVMSLG 237
Db      181  AENLLDADMNKIIDFGPSNEFTVGGKLDITFCGSPPYAABELFGKKYDPEVDVMSLG 240
Qy      238  VLYLVTVSGSLPFDQNLKEIRERVLGRKRYLIPYMSDCEMLIKFLINPSKGTLEQ 297
Db      241  VLYLVTVSGSLPFDQNLKEIRERVLGRKRYLIPYMSDCEMLIKFLINPSKGTLEQ 300
Qy      298  IMKDRMNVVGHEDDELKPYVEPLPDYKDPRTTELMSMGYTRIEIDSLVQRYNEVWAT 357
Db      301  IMKDRMNVVGHEDDELKPYVEPLPDYKDPRTTELMSMGYTRIEIDSLVQRYNEVWAT 360
Qy      358  YLLIGYKSSLEAGDTT-----LKPPASADLTNSAPSPSHKVQSVANPKQRRPSD 410
Db      361  YLLIGYKSSLEAGDTT-----LKPPASADLTNSAPSPSHKVQSVANPKQRRPSD 420
Qy      411  OAGPAIPTNSGYSKKTQSNNAENKRPEDRSRGRKASTAK-----VPASPLPG----- 459
Db      421  HAGPAIPSVAVYPKRSQTSIADGDL-KEDGISRKSQSAVAGGIGIAPASPLGNASPN 479
Qy      460  -----LERKKTPTPTSTNSVLSTSTNSRNSPLERASLGQAS-IQNGKD-STAD-ORVPV 512
Db      480  KADIPERKKSSTVPSNSNTASGAMTRRN-TYVCSRTTADRHSLVQNGKENSITIDQRTPV 538
Qy      513  ASPSAHNSSSGGAPDRNFRGVSSNSTFPAQOLROYRDOQNLPGYVTPASPS-GH--- 568
Db      539  A--STHSISSA-AAPPDIRFPFRGTASRSTFG---OPRERRATYVGPASPISLSHEAT 591
Qy      569  --SQGRGASGISFSKFTSKFVR-RNLNPEPSKDRVETLRPHVVGSGNDKEKEPEAK 625
Db      592  PLSTGRSGSTNLSKLTSLKTRSNVSA-----EQKQENKPAK 630
Qy      626  PRSLRFTWSMKTSSMEPNEMREIRKYLANSQSELEHEKYMLLCMHGTPGHEDFYQWE 685
Db      631  PRSLRFTWSMKTSSMDPGDMREIRKYLANNCDYQREERFLFCVHGQGHENLVQWE 690
Qy      666  MEVCKLPLSLNGVRFRKISGTSMAFKIASKIANELKL 724
Db      691  MEVCKLPLSLNGVRFRKISGTSIAFKNIASKIANELKL 729

RESULT 14
US-09-523-849-33
; Sequence 33, Application US/09523849
; Patent No. 6458561
; GENERAL INFORMATION:

```



```

; APPLICANT: Bandman, Olga
; APPLICANT: Moleent, Angela
; APPLICANT: Magnachi, Paola
; APPLICANT: Bobocci, Roberta
; APPLICANT: Scacchi, Emanuela
; APPLICANT: Isacchi, Antonella
; APPLICANT: Hodgson, Dave
; TITLE OF INVENTION: HUMAN NIM1 KINASE
; FILE REFERENCE: PC-0009 US
; CURRENT APPLICATION NUMBER: US/09/523,849
; CURRENT FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Genbank Accession No. 6458561 G3089349
US-09-523-849-33

Query Match      64.2%; Score 2399; DB 4; Length 729;
Best Local Similarity 66.3%; Pred. No. 1.4e-171;
Matches 503; Conservative 73; Mismatches 115; Indels 68; Gaps 18;

Qy      3 SARTPLPTLNERDTEOPTLGHLDSPSSKSNMIRG---RNS-ATSADQPHIGNYRLK 57
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Db      2 STRPLPTVNERDTEHNT-SHGDRQEVTSRTSRGARCNSIASCADEQPHIGNYRLK 60
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Qy      118 VIETKTLVYMEVYASGGEVFDYLVAGRMKEKEARAKFRQVSAVOYCHQKFIYHBDLK 177
      121 VIETKTLVYIMEVYASGGEVFDYLVAGRMKEKEARAKFRQVSAVOYCHQKFIYHBDLK 180
      178 AENLLDADNMNIKADFGFNEFTFGNKLDTFGSGPPYAAPLFOGKKTGPEVDVWSLG 237
      181 AENLLDADNMNIKADFGFNEFTFGNKLDTFGSGPPYAAPLFOGKKTGPEVDVWSLG 240
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      358 YLLIGYKSELEGDITL-----LKRPSADLTNSAPSPSHKQVSANPKORFSD 410
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      411 QAGPAITSNYSKKTQSNNAENKRPEDRESGRKASTAK-----VPASPLPG----- 459
      421 HAGPAITSVAVYPRRSQTSIADGDL-KEDGISRSKSGSAVGKGIAPAPBMLGNASNP 479
      460 -----LKRKKTTPRTSTSVLSTSTNRNSPFLERASLGQAS-IQNGKD-STAP-QGVV 512
      480 KADIPERKKSSTVSSNTASGGMTRN-TYVCSERTTADRHSHVYQNGKENSITPDQTTVP 538
      513 ASPBANISSSGCAPDRTNPPRGVSSRSTPHAGQLRQVDOQNLPGVTPASP9-GH--- 568
      539 A--STHISISA-ATPDRIRFPRTGASTFPG---OPRERRTATYNGPPASPELSHEAT 591
      569 --SGRGAGASGTSKFTSKFVR-RNLNBPESKORVETLAPHYVVGSGNKGKKEPREAK 625
      592 PLISOTRGRSTNLPSKLTSLKTSKRNVA-----EQDQENKZAK 630
      626 PRSLRFTWMSKTTSSMEPNEMREIRKVLDAANSQSELIHEKYMLLCNHGTTPGHEDFQWE 685
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Qy      686 MEVCKLPRSLNGVRFRRISGTSMAFNIAKSLANLKL 724
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RESULT 15
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; Sequence 8234, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
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; SEQ ID NO 8234
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8234

Query Match      64.1%; Score 2394; DB 4; Length 724;
Best Local Similarity 66.6%; Pred. No. 3.3e-171;
Matches 501; Conservative 73; Mismatches 108; Indels 70; Gaps 18;

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      72 TIGKGNPAKYKLARHLITLGEVAVKIIIDKTQNLSSSLQKLFREVRIMKVLNHPNIVLFE 131
      118 VIETKTLVYMEVYASGGEVFDYLVAGRMKEKEARAKFRQVSAVOYCHQKFIYHBDLK 177
      132 VIETKTLVYIMEVYASGGEVFDYLVAGRMKEKEARAKFRQVSAVOYCHQKFIYHBDLK 191
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      192 AENLLDADNMNIKADFGFNEFTFGNKLDTFGSGPPYAAPLFOGKKTGPEVDVWSLG 251
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      252 VIYTLTVSGSLPPDGNLKLRLERVLGKKYRIPFYMSTDCENLLKFLVLNPSKRGTLQ 311
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      312 IMKDRMNVGHEDDELKPYVEPLPDYKDPRTTELAMSGYTRBEIQDSLVGQRYNEVMAT 371
      358 YLLIGYKSELEGDITLKLKRPADLTNSAPSPSHKQVSANPKORFSDOAGPAIP 417
      372 YLLIGYKSELEGDITLKLKRPADLTNSAPSPSHKQVSANPKORFSDOAGPAIP 422
      418 TSNYSKKTQSNNAENKRPEDRESGRKASTAK-----VPASPLPG-----LER 462
      423 SVAVYPRRSQTSIADGDL-KEDGISRSKSGSAVGKGIAPAPBMLGNASNPKADIPER 481
      463 KKTTPRTSTSVLSTSTNRNSPFLERASLGQAS-IQNGKD-STAP-QGVVAPASPAN 519
      482 KKSSTVSSNTASGGMTRN-TYVCSERTTADRHSHVYQNGKENSITPDQTTVA--STHS 538
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Db 539 ISSA-ATPDRIRFPFGTASRSTFHG---OPRRRTATYNGPPASPISLSHEATPLSQTRS 593
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Db 594 RGSITLFFSKLTSLTRSHVSA-----EQKDNKEAKPRSLRFT 632
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Db 633 WSMKTTSSMBDGDMMREIRKVLIDANNCDYEQRRERFLFCVHGDSHAENLVQWEMEVCKLP 692
QY 693 RLSLNGVRFKRISGTSMAFKNIASKIANELKL 724
Db 693 RLSLNGVRFKRISGTSIAFKNIASKIANELKL 724

Search completed: February 26, 2005, 17:52:59
Job time : 46 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 17:51:28 / Search time 138 Seconds

(without alignments)
1721.045 Million cell updates/sec

Title: US-10-760-407-2

Perfect score: 3737
Sequence: 1 MSARPTPLPTLNRRDTEQPT.....SGTSMARKNIASIKANLKL 724

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubppaa/PCRT_NEW_PUB.pep:*
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- 17: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3737	100.0	724	US-10-274-194-2	Sequence 2, Appl1
2	3737	100.0	724	US-10-760-407-2	Sequence 2, Appl1
3	3736	100.0	724	US-09-919-585-9	Sequence 9, Appl1
4	3670.5	98.2	787	US-10-618-941-76	Sequence 76, Appl1
5	3654	97.8	722	US-10-774-194-4	Sequence 4, Appl1
6	3654	97.8	722	US-10-760-407-4	Sequence 4, Appl1
7	3644	97.5	722	US-08-817-8328-32	Sequence 32, Appl1
8	3644	97.5	722	US-10-440-435-32	Sequence 32, Appl1
9	3566	95.4	691	US-09-919-585-6	Sequence 6, Appl1
10	3515	94.1	745	US-10-195-101-36	Sequence 36, Appl1
11	3515	94.1	745	US-10-161-565-24	Sequence 24, Appl1
12	3515	94.1	745	US-10-260-708-79	Sequence 79, Appl1
13	2555	68.4	793	US-10-195-101-32	Sequence 32, Appl1

14	2552	68.3	795	9	US-09-919-585-12	Sequence 12, Appl1
15	2552	68.3	795	15	US-10-311-034-4	Sequence 4, Appl1
16	2552	68.3	795	17	US-10-753-267-120	Sequence 120, Appl1
17	2546	68.1	795	14	US-10-142-356-9	Sequence 9, Appl1
18	2546	68.1	795	14	US-10-161-565-25	Sequence 25, Appl1
19	2464	65.9	779	8	US-08-817-8328-31	Sequence 31, Appl1
20	2464	65.9	779	15	US-10-440-435-31	Sequence 31, Appl1
21	2419.5	64.7	744	9	US-09-919-585-3	Sequence 3, Appl1
22	2399.5	64.2	744	9	US-09-835-081-4	Sequence 3, Appl1
23	2399	64.2	729	14	US-10-142-356-11	Sequence 11, Appl1
24	2399	64.2	729	14	US-10-195-101-33	Sequence 33, Appl1
25	2399	64.2	729	14	US-10-161-565-26	Sequence 26, Appl1
26	2395.5	64.1	776	15	US-10-366-288-6	Sequence 6, Appl1
27	2381	63.7	713	14	US-10-161-565-27	Sequence 27, Appl1
28	2308	61.8	667	15	US-10-016-248-74	Sequence 74, Appl1
29	2163	57.9	749	15	US-10-333-314-8	Sequence 8, Appl1
30	1940.5	51.9	752	9	US-09-835-081-2	Sequence 2, Appl1
31	1940.5	51.9	752	15	US-10-258-106-16	Sequence 16, Appl1
32	1940.5	51.9	752	15	US-10-276-645-7	Sequence 7, Appl1
33	1940.5	51.9	825	15	US-10-425-114-54516	Sequence 54516, A
34	1936.5	51.8	752	16	US-10-618-941-79	Sequence 79, Appl1
35	1925	51.5	769	15	US-10-363-616-403	Sequence 403, Appl1
36	1913.5	51.2	724	15	US-10-276-645-5	Sequence 5, Appl1
37	1908	51.1	703	15	US-10-016-248-70	Sequence 70, Appl1
38	1878.5	50.3	638	14	US-10-059-585-8	Sequence 8, Appl1
39	1814.5	48.6	698	15	US-10-016-248-22	Sequence 22, Appl1
40	1771	47.4	1038	15	US-10-424-599-274878	Sequence 274878, A
41	1721.5	46.1	688	15	US-10-276-645-8	Sequence 8, Appl1
42	1713.5	45.9	688	14	US-10-161-565-28	Sequence 28, Appl1
43	1713.5	45.9	688	14	US-10-161-565-29	Sequence 29, Appl1
44	1707	45.7	1246	15	US-10-369-493-6585	Sequence 6585, Appl1
45	1693.5	45.3	660	15	US-10-276-645-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-10-274-194-2
Sequence 2, Application US/10274194
Publication No. US20030232408A1
GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THREBOF
FILE REFERENCE: C1001306DIV
CURRENT APPLICATION NUMBER: US/10/274,194
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 724
TYPE: PRT
ORGANISM: Homo sapiens
US-10-274-194-2

Query Match 100.0%; Score 3737; DB 15; Length 724;
Best Local Similarity 100.0%; Pred. No. 1.9e-220;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 MSARPTPLPTLNRRDTEQPTLGHLDKSPSSKSMWINGRNSATSDADQPHGNTRLKTTIG 60
DB 1 MSARPTPLPTLNRRDTEQPTLGHLDKSPSSKSMWINGRNSATSDADQPHGNTRLKTTIG 60
QY 61 KGNFAVKLARHLLTGKEVAVKIIDKTQUNSSSLQKLFREVRIMKVLNHPNIYKLFVIE 120
61 KGNFAVKLARHLLTGKEVAVKIIDKTQUNSSSLQKLFREVRIMKVLNHPNIYKLFVIE 120
DB 61 KGNFAVKLARHLLTGKEVAVKIIDKTQUNSSSLQKLFREVRIMKVLNHPNIYKLFVIE 120
QY 121 TEKTLIVNEVYASGGEVFDVLVHAGRMKEKARAKROVSAVOYCHQKTIYHRDLKAEN 180
121 TEKTLIVNEVYASGGEVFDVLVHAGRMKEKARAKROVSAVOYCHQKTIYHRDLKAEN 180
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Db	161	LLLDADMNKIADFGSNEFTGKMLDTCGSPPYAAPELFOGKXTDGEVDWYSIGVLL	240
QY	241	YTLVSGSLPFDQONLKELEERYLGGXYRIPFWSTSCENLLKKFLLIANSKGTLEQINK	300
Db	241	YTLVSGSLPFDQONLKELEERYLGGXYRIPFWSTSCENLLKKFLLIANSKGTLEQINK	300
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Db	301	DRMNVGHEDDELKPYVEPLPDYKDBRRTLEWVSMGYTREBEIÖDSLVGORYNEVATYLL	360
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QY	421	SYSKKTÖGNNAMENKRPPEEDRESGRVASSPAKYPAASPLPELEKKTPPTSTASVSTSN	480
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QY	481	RSRNSPLIERASLIGASLÖNGKDSIAPÖRFVPVAPSABHNHSSSGGAPDRTNPPRGVSSRS	540
Db	481	RSRNSPLIERASLIGASLÖNGKDSIAPÖRFVPVAPSABHNHSSSGGAPDRTNPPRGVSSRS	540
QY	541	TFHAQQLÖQVDDQÖMLPYGVTPASPSGSHGÖRRGASGSIFSFKTSSKPYVRNNIPEBSKDR	600
Db	541	TFHAQQLÖQVDDQÖMLPYGVTPASPSGSHGÖRRGASGSIFSFKTSSKPYVRNNIPEBSKDR	600
QY	601	VELLRPHVYVSGGANDKEKEEFREAPRSLRFTWSMKTTSSMBPNMREIRKVLJLANSQ	660
Db	601	VELLRPHVYVSGGANDKEKEEFREAPRSLRFTWSMKTTSSMBPNMREIRKVLJLANSQ	660
QY	661	SELHEKYMLLCMHGTPGHEDFVÖWEMEYÖKLPRLSLNGVRFKRISGTSMAFNILASKIAN	720
Db	661	SELHEKYMLLCMHGTPGHEDFVÖWEMEYÖKLPRLSLNGVRFKRISGTSMAFNILASKIAN	720
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Db	721	ELKL 724	

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RESULT 2
US-10-760-407-2
; Sequence 2, Application US/10760407
; Publication No. US20040137499a1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001306-DIV II
; CURRENT APPLICATION NUMBER: US/10/760,407
; CURRENT FILING DATE: 2004-01-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-760-407-2

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Query Match	100.0%	Score 3737	DB 16	Length 724
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Db	1	MSSARPTLPNTNEDTEOPTLGHLDSPSSKSNIRGNATSGADEQPHIGNYRLKTIG	60	
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Db	61	KGSFAKAKLARHLLTGEKVAVKIIDKQLNMSSTIOQLFREIRIMKQLNHPHIVYGLFEVIE	120	

QY	121	TEKTYLYVMEYASGGEVFDYLVAHGMMKEKARAKEROVVASVOYCHOKETVHRDLKAEN	180
Db	121	TEKTYLYVMEYASGGEVFDYLVAHGMMKEKARAKEROVVASVOYCHOKETVHRDLKAEN	180
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QY	241	YTLVSGSLPFDOQNKELRERVLARKYRIPFWMSTDCENLLKKFLILNBSKGTLEQIMK	300
Db	241	YTLVSGSLPFDOQNKELRERVLARKYRIPFWMSTDCENLLKKFLILNBSKGTLEQIMK	300
QY	301	DRMNVVGHEDDELKRYVEPLPYKDPKPRTELVMWNGYTRBEODSLIVGORINEMATYLL	360
Db	301	DRMNVVGHEDDELKRYVEPLPYKDPKPRTELVMWNGYTRBEODSLIVGORINEMATYLL	360
QY	361	LGKXSESEEGDITTLKPPRPSADLTNSSAPSPBHKVORSANPKORRFBDOAGPALPTSN	420
Db	361	LGKXSESEEGDITTLKPPRPSADLTNSSAPSPBHKVORSANPKORRFBDOAGPALPTSN	420
QY	421	SYSKKTOSNNAMENKRPPEEDRESGRYASSTAKVPASPLPGLERKKTTPPTSTNSVLSTSTN	480
Db	421	SYSKKTOSNNAMENKRPPEEDRESGRYASSTAKVPASPLPGLERKKTTPPTSTNSVLSTSTN	480
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Db	661	SELHEKTYLTLCMHGPTGHEDFVQWEMEWECXKLPRLSLNGVRFPRISIGTSMAFNINASKIAN	720
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1  RESULT 3
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3  ; Sequence 9, Application US/09919585
4  ; Patent No. US20020115167A1
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Sun, Tian-Qiang
7  ; APPLICANT: Peng, Jia-Jia
8  ; APPLICANT: Reinhard, Christoph
9  ; APPLICANT: Pantl, Wendy J.
10 ; APPLICANT: Williams, Lewis T.
11 ; TITLE OF INVENTION: ISOLATION OF DROSOPHILA AND HUMAN POLYPEPTIDES ENCODING PAR-1
12 ; TITLE OF INVENTION: POLYPEPTIDES ENCODED BY THE POLYNUCLEOTIDES AND METHODS UTILIZING
13 ; FILE REFERENCE: PP-016093.002/200130.525
14 ; CURRENT APPLICATION NUMBER: US/09/919,585
15 ; CURRENT FILING DATE: 2001-07-30
16 ; NUMBER OF SEQ. ID NOS: 22
17 ; SOFTWARE: FastSeq for Windows Version 4.0
18 ; SEQ ID NO 9
19 ; LENGTH: 724
20 ; TYPE: PRT
21 ; ORGANISM: Homo sapiens
22 ; US-09-919-585-9

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Query Match	100.0%;	Score 3736;	DB 9;	Length 724;
Best Local Similarity	99.9%;	Pred. No. 2.2e-220;		
Matches 723; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;

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      1  MSARPTPLTNERDTEOPTLGHLDSPKSSKSNMIRGNNSATSDAEOPHIGNYRLKLTIG 60
Db      1  MSARPTPLTNERDTEOPTLGHLDSPKSSKSNMIRGNNSATSDAEOPHIGNYRLKLTIG 60
Qy      61  KGNPAKYKLARHILITGKEVAVKIIDKTQLNSSSIQKLFREVRIMKVLNHNHIVLFEVIE 120
      61  KGNPAKYKLARHILITGKEVAVKIIDKTQLNSSSIQKLFREVRIMKVLNHNHIVLFEVIE 120
Db      61  KGNPAKYKLARHILITGKEVAVKIIDKTQLNSSSIQKLFREVRIMKVLNHNHIVLFEVIE 120
Qy      121  TEKTLVYMEYASGGEVFDYLVAGRMKEKAKAFQVAVOYCHQKFIYHDLKAEN 180
      121  TEKTLVYMEYASGGEVFDYLVAGRMKEKAKAFQVAVOYCHQKFIYHDLKAEN 180
Db      121  TEKTLVYMEYASGGEVFDYLVAGRMKEKAKAFQVAVOYCHQKFIYHDLKAEN 180
Qy      181  LLLDADNNIKIADGFSNEFTFGNKLDTFCGSPPYAABELFOGKKYDGPEDVWSLGVTIL 240
      181  LLLDADNNIKIADGFSNEFTFGNKLDTFCGSPPYAABELFOGKKYDGPEDVWSLGVTIL 240
Db      181  LLLDADNNIKIADGFSNEFTFGNKLDTFCGSPPYAABELFOGKKYDGPEDVWSLGVTIL 240
Qy      241  YTLVSGSLPFDGQNLKELRERVLGKYRIPFYMSDCEMLKKFLILNPSKRGTLBQIMK 300
      241  YTLVSGSLPFDGQNLKELRERVLGKYRIPFYMSDCEMLKKFLILNPSKRGTLBQIMK 300
Db      241  YTLVSGSLPFDGQNLKELRERVLGKYRIPFYMSDCEMLKKFLILNPSKRGTLBQIMK 300
Qy      301  DRMMNVGHEDDELKPYVEPLPDYKDPRRTELAMVSMGYTREIODSLVGQRYNEVMATYLL 360
      301  DRMMNVGHEDDELKPYVEPLPDYKDPRRTELAMVSMGYTREIODSLVGQRYNEVMATYLL 360
Db      301  DRMMNVGHEDDELKPYVEPLPDYKDPRRTELAMVSMGYTREIODSLVGQRYNEVMATYLL 360
Qy      361  LDYKSSLEBDTTLKPRPSADLTNSAPSPSHKVQSVSANPKQRFSDOAGPALFTSN 420
      361  LDYKSSLEBDTTLKPRPSADLTNSAPSPSHKVQSVSANPKQRFSDOAGPALFTSN 420
Db      361  LDYKSSLEBDTTLKPRPSADLTNSAPSPSHKVQSVSANPKQRFSDOAGPALFTSN 420
Qy      421  SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLTSTN 480
      421  SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLTSTN 480
Db      421  SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLTSTN 480
Qy      481  RSRNSPLLEBASLGQASIQNGKOSTAQORVPVAPSAHNISSSGGAEDRTNFPBGVSRS 540
      481  RSRNSPLLEBASLGQASIQNGKOSTAQORVPVAPSAHNISSSGGAEDRTNFPBGVSRS 540
Db      481  RSRNSPLLEBASLGQASIQNGKOSTAQORVPVAPSAHNISSSGGAEDRTNFPBGVSRS 540
Qy      541  TFHAGQLRQVRDOONLPYGVTPASPBGSHQGRGASGSIFSKFTSKFVRNLNPEBKDR 600
      541  TFHAGQLRQVRDOONLPYGVTPASPBGSHQGRGASGSIFSKFTSKFVRNLNPEBKDR 600
Db      541  TFHAGQLRQVRDOONLPYGVTPASPBGSHQGRGASGSIFSKFTSKFVRNLNPEBKDR 600
Qy      601  VFTLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPEMMREIRKVLANDANSCQ 660
      601  VFTLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPEMMREIRKVLANDANSCQ 660
Db      601  VFTLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPEMMREIRKVLANDANSCQ 660
Qy      661  SEHHEKXKMLCMGTGPHEDFVQWEMEVCKLPRLSLNGVRFKRIISGTSMAFKQIASKIAN 720
      661  SEHHEKXKMLCMGTGPHEDFVQWEMEVCKLPRLSLNGVRFKRIISGTSMAFKQIASKIAN 720
Db      661  SEHHEKXKMLCMGTGPHEDFVQWEMEVCKLPRLSLNGVRFKRIISGTSMAFKQIASKIAN 720
Qy      721  ELKLT 724
      721  ELKLT 724
Db      721  ELKLT 724

```

RESULT 4

```

US-10-618-941-76
; Sequence 76, Application US/10618941
; Publication No. US2004019792A1
; GENERAL INFORMATION:
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERRARD
; APPLICANT: CAENEPEL, SEAR
; TITLE OF INVENTION: NOVEL KINASES
; FILE REFERENCE: 034536-0321
; CURRENT APPLICATION NUMBER: US/10/618, 941
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/395, 632
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ. ID NOS: 143
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 76
; LENGTH: 787
; TYPE: PRF
; ORGANISM: Homo sapiens

```

US-10-618-941-76

```

Query Match      98.2%; Score 3670.5; DB 16; Length 787;
Best Local Similarity 91.6%; Pred. No. 2,5e-216;
Matches 721; Conservative 1; Mismatches 2; Indels 63; Gaps 2;

```

```

Qy      1  MSARPTPLTNERDTEOPTLGHLDSPKSSKSNMIRGNNSATSDAEOPHIGNYRLKLTIG 60
      1  MSARPTPLTNERDTEOPTLGHLDSPKSSKSNMIRGNNSATSDAEOPHIGNYRLKLTIG 60
Db      1  MSARPTPLTNERDTEOPTLGHLDSPKSSKSNMIRGNNSATSDAEOPHIGNYRLKLTIG 60
Qy      61  KGNPAKYKLARHILITGKEVAVKIIDKTQLNSSSIQKLFREVRIMKVLNHNHIVLFEVIE 120
      61  KGNPAKYKLARHILITGKEVAVKIIDKTQLNSSSIQKLFREVRIMKVLNHNHIVLFEVIE 120
Db      61  KGNPAKYKLARHILITGKEVAVKIIDKTQLNSSSIQKLFREVRIMKVLNHNHIVLFEVIE 120
Qy      121  TEKTLVYMEYASGGEVFDYLVAGRMKEKAKAFQVAVOYCHQKFIYHDLKAEN 180
      121  TEKTLVYMEYASGGEVFDYLVAGRMKEKAKAFQVAVOYCHQKFIYHDLKAEN 180
Db      121  TEKTLVYMEYASGGEVFDYLVAGRMKEKAKAFQVAVOYCHQKFIYHDLKAEN 180
Qy      181  LLLDADNNIKIADGFSNEFTFGNKLDTFCGSPPYAABELFOGKKYDGPEDVWSLGVTIL 240
      181  LLLDADNNIKIADGFSNEFTFGNKLDTFCGSPPYAABELFOGKKYDGPEDVWSLGVTIL 240
Db      181  LLLDADNNIKIADGFSNEFTFGNKLDTFCGSPPYAABELFOGKKYDGPEDVWSLGVTIL 240
Qy      241  YTLVSGSLPFDGQNLKELRERVLGKYRIPFYMSDCEMLKKFLILNPSKRGTLBQIMK 300
      241  YTLVSGSLPFDGQNLKELRERVLGKYRIPFYMSDCEMLKKFLILNPSKRGTLBQIMK 300
Db      241  YTLVSGSLPFDGQNLKELRERVLGKYRIPFYMSDCEMLKKFLILNPSKRGTLBQIMK 300
Qy      301  DRMMNVGHEDDELKPYVEPLPDYKDPRRTELAMVSMGYTREIODSLVGQRYNEVMATYLL 360
      301  DRMMNVGHEDDELKPYVEPLPDYKDPRRTELAMVSMGYTREIODSLVGQRYNEVMATYLL 360
Db      301  DRMMNVGHEDDELKPYVEPLPDYKDPRRTELAMVSMGYTREIODSLVGQRYNEVMATYLL 360
Qy      361  LDYKSSLEBDTTLKPRPSADLTNSAPSPSHKVQSVSANPKQRFSDOAGPALFTSN 420
      361  LDYKSSLEBDTTLKPRPSADLTNSAPSPSHKVQSVSANPKQRFSDOAGPALFTSN 420
Db      361  LDYKSSLEBDTTLKPRPSADLTNSAPSPSHKVQSVSANPKQRFSDOAGPALFTSN 420
Qy      421  SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLTSTN 480
      421  SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLTSTN 480
Db      421  SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLTSTN 480
Qy      481  RSRNSPLLEBASLGQASIQNGKOSTAQORVPVAPSAHNISSSGGAEDRTNFPBGVSRS 540
      481  RSRNSPLLEBASLGQASIQNGKOSTAQORVPVAPSAHNISSSGGAEDRTNFPBGVSRS 540
Db      481  RSRNSPLLEBASLGQASIQNGKOSTAQORVPVAPSAHNISSSGGAEDRTNFPBGVSRS 540
Qy      504  -----STPQORVPVAPSAHNISSSGGAEDRTNFPBGVSRSSTPQAG 546
      504  -----STPQORVPVAPSAHNISSSGGAEDRTNFPBGVSRSSTPQAG 546
Db      541  KASGLPEPTSCNCVPPRSTAPQORVPVAPSAHNISSSGGAEDRTNFPBGVSSTPQAG 600
      541  KASGLPEPTSCNCVPPRSTAPQORVPVAPSAHNISSSGGAEDRTNFPBGVSSTPQAG 600
Qy      547  LRQVRDOONLPYGVTPASPBGSHQGRGASGSIFSKFTSKFV-----RRNLNPEPS 597
      547  LRQVRDOONLPYGVTPASPBGSHQGRGASGSIFSKFTSKFV-----RRNLNPEPS 597
Db      601  LRQVRDOONLPYGVTPASPBGSHQGRGASGSIFSKFTSKFVRNLNPEPS 660
      601  LRQVRDOONLPYGVTPASPBGSHQGRGASGSIFSKFTSKFVRNLNPEPS 660
Qy      598  KDRVETLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPEMMREIRKVLANDAN 657
      598  KDRVETLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPEMMREIRKVLANDAN 657
Db      661  KDRVETLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPEMMREIRKVLANDAN 720
      661  KDRVETLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPEMMREIRKVLANDAN 720
Qy      658  SCQSEHHEKXKMLCMGTGPHEDFVQWEMEVCKLPRLSLNGVRFKRIISGTSMAFKQIASK 717
      658  SCQSEHHEKXKMLCMGTGPHEDFVQWEMEVCKLPRLSLNGVRFKRIISGTSMAFKQIASK 717
Db      721  SCQSEHHEKXKMLCMGTGPHEDFVQWEMEVCKLPRLSLNGVRFKRIISGTSMAFKQIASK 780
      721  SCQSEHHEKXKMLCMGTGPHEDFVQWEMEVCKLPRLSLNGVRFKRIISGTSMAFKQIASK 780
Qy      718  IANELKLT 724
      718  IANELKLT 724
Db      781  IANELKLT 787

```

RESULT 5

```

US-10-274-194-4
; Sequence 4, Application US/10274194
; Publication No. US200303232408A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEIN, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001306DIV

```

;; CURRENT APPLICATION NUMBER: US/10/274,194
;; CURRENT FILING DATE: 2003-12-18
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 4
;; LENGTH: 722
;; TYPE: PR
;; ORGANISM: Rattus norvegicus
US-10-274-194-4

Query Match 97.8%; Score 3654; DB 15; Length 722;
Best Local Similarity 97.8%; Pred. No. 2.3e-215;
Matches 708; Conservative 9; Mismatches 5; Indels 2; Gaps 1;

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QY 1 MSSARTPLPTLNEDTQPTLGHLDKSPSSKSNMIRGNATSADDEPHIGNTRLKTTIG 60
DB 1 MSSARTPLPTLNEDTQPTLGHLDKSPSSKSNMIRGNATSADDEPHIGNTRLKTTIG 60
QY 61 KGNFAKVLARHILITGKEVAVKIIDKTQUNSSLOKLFREVRIMKVLNHNPIVKLFVIE 120
DB 61 KGNFAKVLARHILITGKEVAVKIIDKTQUNSSLOKLFREVRIMKVLNHNPIVKLFVIE 120
QY 121 TEKTLYLMEVYASGGEVFDYLVAHGRMKEKEARAKFRQVSAVOYCHQKFIVHRDLKAEN 180
DB 121 TEKTLYLMEVYASGGEVFDYLVAHGRMKEKEARAKFRQVSAVOYCHQKFIVHRDLKAEN 180
QY 181 LLLDADNMKIKIADPGSFNEFTGKLDTPFGSPPYAAPELFGKKYDDEVDVWSLGVIL 240
DB 181 LLLDADNMKIKIADPGSFNEFTGKLDTPFGSPPYAAPELFGKKYDDEVDVWSLGVIL 240
QY 241 YTLVSGSLPFDQNLKELREVRIRGKYRIPFYMSDCEMLKKFLLINPSKRGTLQIMK 300
DB 241 YTLVSGSLPFDQNLKELREVRIRGKYRIPFYMSDCEMLKKFLLINPSKRGTLQIMK 300
QY 301 DRMMNVGHEDDELKPYVEPLDYKDPRTTELMSMGYTRREIODSLVGQRINEWATYLL 360
DB 301 DRMMNVGHEDDELKPYVEPLDYKDPRTTELMSMGYTRREIODSLVGQRINEWATYLL 360
QY 361 LGYKSSLEEGDTITLKRPSPADLTNSAPSPSHKQSVSANPKQRSDDQAVPAIPTSN 420
DB 361 LGYKSSLEEGDTITLKRPSPADLTNSAPSPSHKQSVSANPKQRSDDQAVPAIPTSN 420
QY 421 SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTTPPTSTNSVLSTSTN 480
DB 421 SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTTPPTSTNSVLSTSTN 480
QY 481 RSRNSPLLEBASLGQASIQNGKDSIAFORVVASPSAHNISSSGAPDRTNFRGVSSRS 540
DB 481 RSRNSPLLEBASLGQASIQNGKDSIAFORVVASPSAHNISSSGAPDRTNFRGVSSRS 540
QY 541 TFHAGQLRQVDOONLPYGVTPASPSGHSQGRGASGIFSKFTSKFVRNINPEPSKOR 600
DB 541 TFHAGQLRQVDOONLPYGVTPASPSGHSQGRGASGIFSKFTSKFVRNINPEPSKOR 600
QY 601 VETLRPHVVGSGGNDKEKEEFREAKPRSLRFTWSMKTTSMEPNEMREIRKVLDA NSCQ 660
DB 601 VETLRPHVVGSGGNDKEKEEFREAKPRSLRFTWSMKTTSMEPNEMREIRKVLDA NSCQ 660
QY 661 SELHEKYMLLCMHGTGPHGDFVQWEMEVCKLPRLSLNGVRFKRISGTSMAFKNIASIXAN 720
DB 661 SELHEKYMLLCMHGTGPHGDFVQWEMEVCKLPRLSLNGVRFKRISGTSMAFKNIASIXAN 720
QY 721 ELKL 724
DB 719 ELKL 722
```

RESULT 6
US-10-760-407-4
; Sequence 4, Application US/10760407
; Publication No. US20040137499A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.

;; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;; FILE OF INVENTION: THEREOF
;; FILE REFERENCE: C1001306-DIV II
;; CURRENT APPLICATION NUMBER: US/10/760,407
;; CURRENT FILING DATE: 2004-01-21
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 4
;; LENGTH: 722
;; TYPE: PR
;; ORGANISM: Rattus norvegicus
US-10-760-407-4

Query Match 97.8%; Score 3654; DB 16; Length 722;
Best Local Similarity 97.8%; Pred. No. 2.3e-215;
Matches 708; Conservative 9; Mismatches 5; Indels 2; Gaps 1;

```
QY 1 MSSARTPLPTLNEDTQPTLGHLDKSPSSKSNMIRGNATSADDEPHIGNTRLKTTIG 60
DB 1 MSSARTPLPTLNEDTQPTLGHLDKSPSSKSNMIRGNATSADDEPHIGNTRLKTTIG 60
QY 61 KGNFAKVLARHILITGKEVAVKIIDKTQUNSSLOKLFREVRIMKVLNHNPIVKLFVIE 120
DB 61 KGNFAKVLARHILITGKEVAVKIIDKTQUNSSLOKLFREVRIMKVLNHNPIVKLFVIE 120
QY 121 TEKTLYLMEVYASGGEVFDYLVAHGRMKEKEARAKFRQVSAVOYCHQKFIVHRDLKAEN 180
DB 121 TEKTLYLMEVYASGGEVFDYLVAHGRMKEKEARAKFRQVSAVOYCHQKFIVHRDLKAEN 180
QY 181 LLLDADNMKIKIADPGSFNEFTGKLDTPFGSPPYAAPELFGKKYDDEVDVWSLGVIL 240
DB 181 LLLDADNMKIKIADPGSFNEFTGKLDTPFGSPPYAAPELFGKKYDDEVDVWSLGVIL 240
QY 241 YTLVSGSLPFDQNLKELREVRIRGKYRIPFYMSDCEMLKKFLLINPSKRGTLQIMK 300
DB 241 YTLVSGSLPFDQNLKELREVRIRGKYRIPFYMSDCEMLKKFLLINPSKRGTLQIMK 300
QY 301 DRMMNVGHEDDELKPYVEPLDYKDPRTTELMSMGYTRREIODSLVGQRINEWATYLL 360
DB 301 DRMMNVGHEDDELKPYVEPLDYKDPRTTELMSMGYTRREIODSLVGQRINEWATYLL 360
QY 361 LGYKSSLEEGDTITLKRPSPADLTNSAPSPSHKQSVSANPKQRSDDQAVPAIPTSN 420
DB 361 LGYKSSLEEGDTITLKRPSPADLTNSAPSPSHKQSVSANPKQRSDDQAVPAIPTSN 420
QY 421 SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTTPPTSTNSVLSTSTN 480
DB 421 SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTTPPTSTNSVLSTSTN 480
QY 481 RSRNSPLLEBASLGQASIQNGKDSIAFORVVASPSAHNISSSGAPDRTNFRGVSSRS 540
DB 481 RSRNSPLLEBASLGQASIQNGKDSIAFORVVASPSAHNISSSGAPDRTNFRGVSSRS 540
QY 541 TFHAGQLRQVDOONLPYGVTPASPSGHSQGRGASGIFSKFTSKFVRNINPEPSKOR 600
DB 541 TFHAGQLRQVDOONLPYGVTPASPSGHSQGRGASGIFSKFTSKFVRNINPEPSKOR 600
QY 601 VETLRPHVVGSGGNDKEKEEFREAKPRSLRFTWSMKTTSMEPNEMREIRKVLDA NSCQ 660
DB 601 VETLRPHVVGSGGNDKEKEEFREAKPRSLRFTWSMKTTSMEPNEMREIRKVLDA NSCQ 660
QY 661 SELHEKYMLLCMHGTGPHGDFVQWEMEVCKLPRLSLNGVRFKRISGTSMAFKNIASIXAN 720
DB 661 SELHEKYMLLCMHGTGPHGDFVQWEMEVCKLPRLSLNGVRFKRISGTSMAFKNIASIXAN 720
QY 721 ELKL 724
DB 719 ELKL 722
```

RESULT 7
US-08-817-832B-32

```

; Sequence 32, Application US/08817832B
; Publication No. US20030104516A1
; GENERAL INFORMATION:
; APPLICANT: MANDELKOW, Eckhard, et al.
; TITLE OF INVENTION: No. US20030104516A1 Protein Kinase (NPK-110)
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 S. Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: US
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,832B
; FILING DATE: 28-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/04258
; FILING DATE: 30-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94 11 7122.5
; FILING DATE: 28-OCT-1994
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 722 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-817-832B-32

```

Query Match 97.5%; Score 3644; DB 8; Length 722;

Best Local Similarity 97.5%; Pred. No. 9.5e-215;

Matches 706; Conservative 9; Mismatches 7; Indels 2; Gaps 1;

```

QY 1 MSSARTPLPTLNERTDEOPTLGHLDSPSSKSNMIRGNSATSADDEQPHIGNYRLKTTIG 60
DB 1 MSSARTPLPTLNERTDEOPTLGHLDSPSSKSNMIRGNSATSADDEQPHIGNYRLKTTIG 60
QY 61 KGNPAKYKLARHILTGKAVAVKIIDKTQLNSSLQKLPREVRIMKVLNHPNIVKLEFVIE 120
DB 61 KGNPAKYKLARHILTGKAVAVKIIDKTQLNSSLQKLPREVRIMKVLNHPNIVKLEFVIE 120
QY 121 TEKTLVLMVEYASGGEVFDVLVAHGRMKEKARAKFRQVSAVOYCHHKFIYHRDLKAEN 180
DB 121 TEKTLVLMVEYASGGEVFDVLVAHGRMKEKARAKFRQVSAVOYCHHKFIYHRDLKAEN 180
QY 181 LLLDADNNIKIADFGFNEFTFGNKLDTFCGSPPYAAPLFOGKKYDGPEDVWSLGVIL 240
DB 181 LLLDADNNIKIADFGFNEFTFGNKLDTFCGSPPYAAPLFOGKKYDGPEDVWSLGVIL 240
QY 241 YTLVSGSLPFDGQNLKELREVRILGKRIPIYMSDCEMLIKFLLINPSKRGTLGDIWK 300
DB 241 YTLVSGSLPFDGQNLKELREVRILGKRIPIYMSDCEMLIKFLLINPSKRGTLGDIWK 300
QY 301 DRMMNVGHEDDELKPYEPLPDYKDPRTTELVMVSGYTRBEIDSLVGOYVEMVATYLL 360
DB 301 DRMMNVGHEDDELKPYEPLPDYKDPRTTELVMVSGYTRBEIDSLVGOYVEMVATYLL 360
QY 361 LGYKSELLEGDTITLKRPSPADLTNSGAPSPSHKQSVSANPKQRRFSDQAGPAIPTSN 420
DB 361 LGYKSELLEGDTITLKRPSPADLTNSGAPSPSHKQSVSANPKQRRFSDQAGPAIPTSN 420
QY 421 SYGKTKOSNNAENKRPEDRSBGKASTAKVAPASPLPGLEBKKTTPPTSTNSVLTSTN 480
DB 421 SYGKTKOSNNAENKRPEDRSBGKASTAKVAPASPLPGLEBKKTTPPTSTNSVLTSTN 480
QY 481 RSRNSPLERASLGOASIQNGKOSTAPQRPVVASPSAHNITSSSGGADPRTNPPGVSRS 540
DB 481 RSRNSPLERASLGOASIQNGKOSTAPQRPVVASPSAHNITSSSGGADPRTNPPGVSRS 540

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DB 479 RSRNSPLERASLGOASIQNGKOSTAPQRPVVASPSAHNITSSSGGADPRTNPPGVSRS 538
QY 541 TFHAGQLRQVRDQNLPEYGVTPASPSSGSGRRGASGIFSFKPTSKFVRRLNPESSKDR 600
DB 539 TFHAGQLRQVRDQNLPEYGVTPASPSSGSGRRGASGIFSFKPTSKFVRRLNPESSKDR 598
QY 601 VETLRPRVVGSGNDEKEEFREKPRSLAFTYMSMKTSSMEPEMREIRKVLDA NSCQ 660
DB 599 VETLRPRVVGSGNDEKEEFREKPRSLAFTYMSMKTSSMEPEMREIRKVLDA NSCQ 658
QY 661 SELHEKYMLCMEGTPEGHDFVQWEMEVCKLPRLSLNGVFPKRSIGTSMFKNYASXTAN 720
DB 659 SELHEKYMLCMEGTPEGHDFVQWEMEVCKLPRLSLNGVFPKRSIGTSMFKNYASXTAN 718
QY 721 ELKL 724
DB 719 ELKL 722

```

RESULT 8

US-10-440-435-32

; Sequence 32, Application US/10440435

; Publication No. US20040038361A1

; GENERAL INFORMATION:

; APPLICANT: MANDELKOW, Eckhard, et al.

; TITLE OF INVENTION: No. US20040038361A1 Protein Kinase (NPK-110)

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 233 S. Wacker Drive, 6300 Sears Tower

; CITY: Chicago

; STATE: Illinois

; COUNTRY: US

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/440,435

; FILING DATE: 16-May-2003

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/EP95/04258

; FILING DATE: 30-OCT-1995

; APPLICATION NUMBER: EP 94 11 7122.5

; FILING DATE: 28-OCT-1994

; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 722 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 32:

US-10-440-435-32

Query Match 97.5%; Score 3644; DB 15; Length 722;

Best Local Similarity 97.5%; Pred. No. 9.5e-215;

Matches 706; Conservative 9; Mismatches 7; Indels 2; Gaps 1;

```

QY 1 MSSARTPLPTLNERTDEOPTLGHLDSPSSKSNMIRGNSATSADDEQPHIGNYRLKTTIG 60
DB 1 MSSARTPLPTLNERTDEOPTLGHLDSPSSKSNMIRGNSATSADDEQPHIGNYRLKTTIG 60
QY 61 KGNPAKYKLARHILTGKAVAVKIIDKTQLNSSLQKLPREVRIMKVLNHPNIVKLEFVIE 120
DB 61 KGNPAKYKLARHILTGKAVAVKIIDKTQLNSSLQKLPREVRIMKVLNHPNIVKLEFVIE 120
QY 121 TEKTLVLMVEYASGGEVFDVLVAHGRMKEKARAKFRQVSAVOYCHHKFIYHRDLKAEN 180
DB 121 TEKTLVLMVEYASGGEVFDVLVAHGRMKEKARAKFRQVSAVOYCHHKFIYHRDLKAEN 180

```

QY 181 LLLDADNMNLIKADFGFSNEFTGKNLDTFCGSPPYAAPELFOGKKYDGEVDWMSLVYL 240
DB 181 LLLDADNMNLIKADFGFSNEFTGKNLDTFCGSPPYAAPELFOGKKYDGEVDWMSLVYL 240
QY 241 YTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMGSTDCENLLKKFLINPSKRGTLQOIMK 300
DB 241 YTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMGSTDCENLLKKFLINPSKRGTLQOIMK 300
QY 301 DRMNNGHEDDELKPYVEPLPDYDQDPRTELVMGKGTREIQLSLVGQRYNEWATYLL 360
DB 301 DRMNNGHEDDELKPYVEPLPDYDQDPRTELVMGKGTREIQLSLVGQRYNEWATYLL 360
QY 361 LGYSSELEGGDTITLKPRPSADLTNSSAPSPSHVQSVSANPKORRPFSDQAGPATPSN 420
DB 361 LGYSSELEGGDTITLKPRPSADLTNSSAPSPSHVQSVSANPKORRPFSDQAGPATPSN 420
QY 421 SYSKTOSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLTSTN 480
DB 421 SYSKTOSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLTSTN 480
QY 481 RSRNSPLERASLGQASTIQNGKDTAPQRPVAPSPSAHNTSSSGADRTNPFRCVSSRS 540
DB 479 RSRNSPLERASLGQASTIQNGKDTAPQRPVAPSPSAHNTSSSGADRTNPFRCVSSRS 538
QY 541 TFHAGOLROYDQONLPEYVTPASPSSGSGRGAAGSIFSKFTSKFVRNLNBPESKDR 600
DB 539 TFHAGOLROYDQONLPEYVTPASPSSGSGRGAAGSIFSKFTSKFVRNLNBPESKDR 598
QY 601 VETLRPHVVGSGGNDKEKEEFREAKPRSLRPTMSMKTTSMEPEMNRIRKVLANSQ 660
DB 599 VETLRPHVVGSGGNDKEKEEFREAKPRSLRPTMSMKTTSMEPEMNRIRKVLANSQ 658
QY 661 SELHEKTMLCMHGTPEGHEDFVQWEMEVCKLPRLSLNGVRFKRLSGTSMAPKNIASRTAN 720
DB 659 SELHEKTMLCMHGTPEGHEDFVQWEMEVCKLPRLSLNGVRFKRLSGTSMAPKNIASRTAN 718
QY 721 ELKL 724
DB 719 ELKL 722

RESULT 9
US-09-919-585-6
Sequence 6, Application US/09919585
Patent No. US20020115167A1
GENERAL INFORMATION:
APPLICANT: Sun, Tian-Qiang
APPLICANT: Feng, Jia-Jia
APPLICANT: Reinhard, Christoph
APPLICANT: Fanti, Wendy J.
APPLICANT: Williams, Lewis T.
TITLE OF INVENTION: ISOLATION OF DROSOPHILA AND HUMAN POLYNUCLEOTIDES ENCODING PAR-1
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES
FILE REFERENCE: PP-016093.002/200130.525
CURRENT APPLICATION NUMBER: US/09/919,585
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 691
TYPE: PRT
ORGANISM: Homo sapiens
US-09-919-585-6

Query Match 95.4%; Score 3566; DB 9; Length 691;
Best Local Similarity 99.9%; Pred. No. 5.4e-210;
Matches 690; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 34 MIRGRSATSADBPPIGNRYRLKTIQGNFAKVLARHLNGKEVAVKIIDKTOUNSSS 93
DB 1 MIRGRSATSADBPPIGNRYRLKTIQGNFAKVLARHLNGKEVAVKIIDKTOUNSSS 60

QY 94 LQKLPREVRIMKVLNPNVTKLPEVETEKTLYLWERYASGGHVPYLYAHGMEKEKAR 153
DB 61 LQKLPREVRIMKVLNPNVTKLPEVETEKTLYLWERYASGGHVPYLYAHGMEKEKAR 120
QY 154 AKFRQVSAVOYCHQKFIYHRDLKAEMLLLDADNMNLIKADFGFSNEFTGKNLDTFCGSP 213
DB 121 AKFRQVSAVOYCHQKFIYHRDLKAEMLLLDADNMNLIKADFGFSNEFTGKNLDTFCGSP 180
QY 214 PYAAPELFOGKKYDGEVDWMSLVYLITLVSGSLPFDGQNLKELRERVLRGKYRIPFYM 273
DB 181 PYAAPELFOGKKYDGEVDWMSLVYLITLVSGSLPFDGQNLKELRERVLRGKYRIPFYM 240
QY 274 STDCEMLKKFLINPSKRGTLQOIMKDMNNGHEDDELKPYVEPLPDYDQDPRTELVMY 333
DB 241 STDCEMLKKFLINPSKRGTLQOIMKDMNNGHEDDELKPYVEPLPDYDQDPRTELVMY 300
QY 334 SMGTYREIQLSLVGQRYNEWATYLLLGYSSELEGGDTITLKPRPSADLTNSSAPSPSH 393
DB 301 SMGTYREIQLSLVGQRYNEWATYLLLGYSSELEGGDTITLKPRPSADLTNSSAPSPSH 360
QY 394 KYQSVSANPKORRPSDQAGPALPTNSYSKKTQSNNAENKRPEDRESGRKASTAKVP 453
DB 361 KYQSVSANPKORRPSDQAGPALPTNSYSKKTQSNNAENKRPEDRESGRKASTAKVP 420
QY 454 ASPLPGLERKKTPTPTSTNSVLTSTNSRNSPLERASLGQASTIQNGKDTAPQRPVPA 513
DB 421 ASPLPGLERKKTPTPTSTNSVLTSTNSRNSPLERASLGQASTIQNGKDTAPQRPVPA 480
QY 514 SPSAHNTSSSGADRTNPFRCVSSRSTFHAGOLROYDQONLPEYVTPASPSSGSGR 573
DB 481 SPSAHNTSSSGADRTNPFRCVSSRSTFHAGOLROYDQONLPEYVTPASPSSGSGR 540
QY 574 GASGSIFSKFTSKFVRNLNBPESKORVETLRPHVVGSGGNDKEKEEFREAKPRSLRPTW 633
DB 541 GASGSIFSKFTSKFVRNLNBPESKORVETLRPHVVGSGGNDKEKEEFREAKPRSLRPTW 600
QY 634 SMKTTSMEPEMNRIRKVLANSQSELEHKYWLICMHGTPEGHEDFVQWEMEVCKLP 693
DB 601 SMKTTSMEPEMNRIRKVLANSQSELEHKYWLICMHGTPEGHEDFVQWEMEVCKLP 660
QY 694 ISLNGVRFKRLSGTSMAPKNIASKIANELKL 724
DB 661 ISLNGVRFKRLSGTSMAPKNIASKIANELKL 691

RESULT 10
US-10-195-101-36
Sequence 36, Application US/10195101
Publication No. US20030087317A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Molteni, Angela
APPLICANT: Magnaghi, Paola
APPLICANT: Bosotti, Roberta
APPLICANT: Scaccheri, Emanuela
APPLICANT: Isacchi, Antonella
APPLICANT: Hodgson, David M.
TITLE OF INVENTION: HUMAN NIMA KINASE
FILE REFERENCE: PC-0009-1 CIP
CURRENT APPLICATION NUMBER: US/10/195,101
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: 09/523,849
PRIOR FILING DATE: 2000-03-13
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PERL Program
SEQ ID NO 36
LENGTH: 745
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: misc. feature
NAME/KEY: GenBank Accession No. US20030087317A1 g1749794
OTHER INFORMATION: GenBank

DATABASE ENTRY DATE: 1 October 1998
US-10-195-101-36

Query Match 94.1%; Score 3515; DB 14; Length 745;
Best Local Similarity 92.3%; Pred. No. 7.8e-207;
Matches 688; Conservative 1; Mismatches 2; Indels 54; Gaps 1;

QY 34 MINGRNSATSADBPPIGNRLIKTIGKGNPAKYLARHILITGKEVAVKIIDKTQNLSSS 93
DB 1 MINGRNSATSADBPPIGNRLIKTIGKGNPAKYLARHILITGKEVAVKIIDKTQNLSSS 60
QY 94 LQKLFREVRIMKVLNHPNIVKLFEVITEKTLVLMVEYASGGEVFDVLVHGRMKEAR 153
DB 61 LQKLFREVRIMKVLNHPNIVKLFEVITEKTLVLMVEYASGGEVFDVLVHGRMKEAR 120
QY 154 AKRQVSAVQYCHQKFIYHRDLKAENLLDADMNLIKADFGSNEFTFGNKLDTFCGSP 213
DB 121 AKRQVSAVQYCHQKFIYHRDLKAENLLDADMNLIKADFGSNEFTFGNKLDTFCGSP 180
QY 214 PYAAPBLFOGKYDGPEDVWSLGVILYTLVSGSLPFDGQNLKELRERVLRGKXRIPFYM 273
DB 181 PYAAPBLFOGKYDGPEDVWSLGVILYTLVSGSLPFDGQNLKELRERVLRGKXRIPFYM 240
QY 274 STDCENLLKKFLLINPSKGTLEQIMKDRMNVGHEDDELKPYVEPLPDYKDPRTTELAV 333
DB 241 STDCENLLKKFLLINPSKGTLEQIMKDRMNVGHEDDELKPYVEPLPDYKDPRTTELAV 300
QY 334 SMGYTREIODSLVGORYNEVMATYLLGYKSSLEBDITTLKRPASADLTNSASPSH 393
DB 301 SMGYTREIODSLVGORYNEVMATYLLGYKSSLEBDITTLKRPASADLTNSASPSH 360
QY 394 KVORSVANPKORRFSQAGPAIPTNSYSKKTOSNNAENKRPEDRESGRKASSTAKVP 453
DB 361 KVORSVANPKORRFSQAGPAIPTNSYSKKTOSNNAENKRPEDRESGRKASSTAKVP 420
QY 454 ASPLPGLERKKTPTPTSTNSVLSTSTNRSNPSLLERASLGQASIQNGKX----- 503
DB 421 ASPLPGLERKKTPTPTSTNSVLSTSTNRSNPSLLERASLGQASIQNGKX----- 480
QY 504 -----STAPORVPVAPSAHN 519
DB 481 TASASAANVSAARPROHOKMSASAVHPNKASGLPPTESNCEVPRPSTAPQRPVAPSAHN 540
QY 520 ISSSGAPDRTNPRGVSSRSTFHAQLRQVRDOQLPYGVTPASPSGHSQGRGASGI 579
DB 541 ISSSGAPDRTNPRGVSSRSTFHAQLRQVRDOQLPYGVTPASPSGHSQGRGASGI 600
QY 580 FSKFTSKFVRRLNNEPESKDRVETLARPHVVGSGNDKEKEEPREAKRSLRFTWSMKTT 639
DB 601 FSKFTSKFVRRLNNEPESKDRVETLARPHVVGSGNDKEKEEPREAKRSLRFTWSMKTT 660
QY 640 SMEPNEMREIRKVLNDSQSELEHKEYMLLCHGTFPGHEDFVQWEMEVCCKLRLSLNGV 699
DB 661 SMEPNEMREIRKVLNDSQSELEHKEYMLLCHGTFPGHEDFVQWEMEVCCKLRLSLNGV 720
QY 700 RPKRISGTSMAFNKIASKIANKL 724
DB 721 RPKRISGTSMAFNKIASKIANKL 745

RESULT 11
US-10-161-565-24
; Sequence 24, Application US/10161565
; Publication No. US20030165809A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: MARKS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-086C
; CURRENT APPLICATION NUMBER: US/10/161,565
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605

PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/357,253
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 745
TYPE: PRF
ORGANISM: Homo sapiens
US-10-161-565-24

Query Match 94.1%; Score 3515; DB 14; Length 745;
Best Local Similarity 92.3%; Pred. No. 7.8e-207;
Matches 688; Conservative 1; Mismatches 2; Indels 54; Gaps 1;

QY 34 MINGRNSATSADBPPIGNRLIKTIGKGNPAKYLARHILITGKEVAVKIIDKTQNLSSS 93
DB 1 MINGRNSATSADBPPIGNRLIKTIGKGNPAKYLARHILITGKEVAVKIIDKTQNLSSS 60
QY 94 LQKLFREVRIMKVLNHPNIVKLFEVITEKTLVLMVEYASGGEVFDVLVHGRMKEAR 153
DB 61 LQKLFREVRIMKVLNHPNIVKLFEVITEKTLVLMVEYASGGEVFDVLVHGRMKEAR 120
QY 154 AKRQVSAVQYCHQKFIYHRDLKAENLLDADMNLIKADFGSNEFTFGNKLDTFCGSP 213
DB 121 AKRQVSAVQYCHQKFIYHRDLKAENLLDADMNLIKADFGSNEFTFGNKLDTFCGSP 180
QY 214 PYAAPBLFOGKYDGPEDVWSLGVILYTLVSGSLPFDGQNLKELRERVLRGKXRIPFYM 273
DB 181 PYAAPBLFOGKYDGPEDVWSLGVILYTLVSGSLPFDGQNLKELRERVLRGKXRIPFYM 240
QY 274 STDCENLLKKFLLINPSKGTLEQIMKDRMNVGHEDDELKPYVEPLPDYKDPRTTELAV 333
DB 241 STDCENLLKKFLLINPSKGTLEQIMKDRMNVGHEDDELKPYVEPLPDYKDPRTTELAV 300
QY 334 SMGYTREIODSLVGORYNEVMATYLLGYKSSLEBDITTLKRPASADLTNSASPSH 393
DB 301 SMGYTREIODSLVGORYNEVMATYLLGYKSSLEBDITTLKRPASADLTNSASPSH 360
QY 394 KVORSVANPKORRFSQAGPAIPTNSYSKKTOSNNAENKRPEDRESGRKASSTAKVP 453
DB 361 KVORSVANPKORRFSQAGPAIPTNSYSKKTOSNNAENKRPEDRESGRKASSTAKVP 420
QY 454 ASPLPGLERKKTPTPTSTNSVLSTSTNRSNPSLLERASLGQASIQNGKX----- 503
DB 421 ASPLPGLERKKTPTPTSTNSVLSTSTNRSNPSLLERASLGQASIQNGKX----- 480
QY 504 -----STAPORVPVAPSAHN 519
DB 481 TASASAANVSAARPROHOKMSASAVHPNKASGLPPTESNCEVPRPSTAPQRPVAPSAHN 540
QY 520 ISSSGAPDRTNPRGVSSRSTFHAQLRQVRDOQLPYGVTPASPSGHSQGRGASGI 579
DB 541 ISSSGAPDRTNPRGVSSRSTFHAQLRQVRDOQLPYGVTPASPSGHSQGRGASGI 600
QY 580 FSKFTSKFVRRLNNEPESKDRVETLARPHVVGSGNDKEKEEPREAKRSLRFTWSMKTT 639
DB 601 FSKFTSKFVRRLNNEPESKDRVETLARPHVVGSGNDKEKEEPREAKRSLRFTWSMKTT 660
QY 640 SMEPNEMREIRKVLNDSQSELEHKEYMLLCHGTFPGHEDFVQWEMEVCCKLRLSLNGV 699
DB 661 SMEPNEMREIRKVLNDSQSELEHKEYMLLCHGTFPGHEDFVQWEMEVCCKLRLSLNGV 720
QY 700 RPKRISGTSMAFNKIASKIANKL 724
DB 721 RPKRISGTSMAFNKIASKIANKL 745

RESULT 12
US-10-260-708-79
; Sequence 79, Application US/10260708
; Publication No. US20040063101A1
; GENERAL INFORMATION:

```

; APPLICANT: Scanlan, Matthew
; APPLICANT: Lee, Sang-Yull
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Human Sarcoma-Associated Antigens
; FILE REFERENCE: L00461/70138
; CURRENT APPLICATION NUMBER: US/10/260,708
; CURRENT FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 745
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-260-708-79

Query Match      94.1%; Score 3515; DB 15; Length 745;
Best Local Similarity 92.3%; Pred. No. 7.8e-207;
Matches 688; Conservative 1; Mismatches 2; Indels 54; Gaps 1;

Qy      34  MIRGNATSADQPHIGNYRLKTIGKGNPAKYKLARHILTYGEVAVKIIIDKTQINSSS 93
      |||
Db      1  MIRGNATSADQPHIGNYRLKTIGKGNPAKYKLARHILTYGEVAVKIIIDKTQINSSS 60
Qy      94  LQKLFREVRIMKVLNHPNIVKLFVIEITEKTYLWMEVASGGEVFDYLVAGRMKEKEAR 153
      |||
Db      61  LQKLFREVRIMKVLNHPNIVKLFVIEITEKTYLWMEVASGGEVFDYLVAGRMKEKEAR 120
Qy      154 AKPRQVSAVOYCHQKTIYHRDLKAENLLDADNNIKIADPGSNETFGNKLDTFGCGSP 213
      |||
Db      121 AKPRQVSAVOYCHQKTIYHRDLKAENLLDADNNIKIADPGSNETFGNKLDTFGCGSP 180
Qy      214 PYAPBELFOGKYDGPEDVWVSLGVILYTVSGSLPPDQONLKELRERVLRGKYRIPEYM 273
      |||
Db      181 PYAPBELFOGKYDGPEDVWVSLGVILYTVSGSLPPDQONLKELRERVLRGKYRIPEYM 240
Qy      274 STDCENLKKFPLINPSKRGTLQIIMKORMNNGHEDDELKPYEPLPDYKDPRTRELMV 333
      |||
Db      241 STDCENLKKFPLINPSKRGTLQIIMKORMNNGHEDDELKPYEPLPDYKDPRTRELMV 300
Qy      334 SMGVTREIDSLVGRVYNEVMAVYLLGYKSELEBDTTLTKPRPADITNSASPSH 393
      |||
Db      301 SMGVTREIDSLVGRVYNEVMAVYLLGYKSELEBDTTLTKPRPADITNSASPSH 360
Qy      394 KVQRSVANPKORFSDQAGPAIPTNSYSKKTQSNNAENKRPEDDESGRKASSTAKYV 453
      |||
Db      361 KVQRSVANPKORFSDQAGPAIPTNSYSKKTQSNNAENKRPEDDESGRKASSTAKYV 420
Qy      454 ASPLPGLERKKTPTPESTNSVLTSTNRSNPSPLERASTIGQASIONGKD----- 503
      |||
Db      421 ASPLPGLERKKTPTPESTNSVLTSTNRSNPSPLERASTIGQASIONGKSLTMPGSRAS 480
Qy      504 -----STAPQVRVPAASPSAN 519
      |||
Db      481 TASASAASVAPRROHOKSMASAVHPNKASGLPPTESNCEVPPSTAPQVRVPAASPSAN 540
Qy      520 ISSSGAGPDRFTNPRGVSSRSTFHAQRLQVRDQONLPGVTPASPSGSGRGAAGS 579
      |||
Db      541 ISSSGAGPDRFTNPRGVSSRSTFHAQRLQVRDQONLPGVTPASPSGSGRGAAGS 600
Qy      580 FSKFTSKFVARNINPEPSKQVETLAPHYVSGGNDKKEEFREAPRSILRFTWSMKTTS 639
      |||
Db      601 FSKFTSKFVARNINPEPSKQVETLAPHYVSGGNDKKEEFREAPRSILRFTWSMKTTS 660
Qy      640 SMEPNEMREIRKVLANSQSELEHEKVMLCMGHTPGHEDFVQMEVEXCKLPRSLINLV 699
      |||
Db      661 SMEPNEMREIRKVLANSQSELEHEKVMLCMGHTPGHEDFVQMEVEXCKLPRSLINLV 720
Qy      700 RFRRIISGTSMAFNINASKIANELKLT 724
      |||
Db      721 RFRRIISGTSMAFNINASKIANELKLT 745

RESULT 13
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US-10-195-101-32
; Sequence 32, Application US/10195101
; Publication No. US20030087317A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Molteni, Angela
; APPLICANT: Magnaghi, Paola
; APPLICANT: Bobetti, Roberta
; APPLICANT: Scacheri, Emanuela
; APPLICANT: Isacchi, Antonella
; APPLICANT: Hodgson, David M.
; TITLE OF INVENTION: HUMAN NIM1 KINASE
; FILE REFERENCE: PC-0009-1 CIP
; CURRENT APPLICATION NUMBER: US/10/195,101
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: 09/523,849
; PRIOR FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PERL Program
; SEQ ID NO 32
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank Accession No. US20030087317A1 G2052189
US-10-195-101-32

Query Match      68.4%; Score 2555; DB 14; Length 793;
Best Local Similarity 65.5%; Pred. No. 4.9e-148;
Matches 525; Conservative 82; Mismatches 105; Indels 90; Gaps 14;

Qy      3  SARTPLPTINERDTEQPTL--GHLD-----SKPSSKSNMIRGNATSQA-DEQPHIGNYR 54
      |||
Db      2  SARTPLPTINERDTEINHTSVSDGYETTHIIPTKSSSRQNIPCRNSITSATDEQPHIGNYR 61
Qy      55  LKKTIGKGNPAKYKLARHILTYGEVAVKIIIDKTQINSSSLQKLFREVRIMKVLNHPNIVK 114
      |||
Db      62  LKKTIGKGNPAKYKLARHILTYGEVAVKIIIDKTQINPSLQKLFREVRIMKVLNHPNIVK 121
Qy      115  LFEVIEITEKTYLWMEVASGGEVFDYLVAGRMKEKEARAKFRQVSAVOYCHQKTIYHR 174
      |||
Db      122  LFEVIEITEKTYLWMEVASGGEVFDYLVAGRMKEKEARAKFRQVSAVOYCHQKTIYHR 181
Qy      175  DKAENLLDADNNIKIADPGFSNEFTGNTKLDTFGCGSPPYAPBELFOGKYDGPEDVWV 234
      |||
Db      182  DKAENLLDADNNIKIADPGFSNEFTGNTKLDTFGCGSPPYAPBELFOGKYDGPEDVWV 241
Qy      235  SLGVILYTVSGSLPPDQONLKELRERVLRGKYRIPEYMSSTDCENLKKFPLINPSKRG 294
      |||
Db      242  SLGVILYTVSGSLPPDQONLKELRERVLRGKYRIPEYMSSTDCENLKKFPLINPSKRG 301
Qy      295  LEQIMKORMNNGVGHEDDELKPYEPLPDYKDPRTRELMVSMGVTREIDSLVGRVYNEV 354
      |||
Db      302  LEQIMKORMNNGVGHEDDELKPYEPLPDYKDPRTRELMVSMGVTREIDSLVGRVYNEV 361
Qy      355  MATYLLILGYKSELEB-----DTTLTKPRPADITNSASPSH-KVQRSVANPKORR 407
      |||
Db      362  MATYLLILGRKPEEGGSLSSGNLCQSRSSDILNNTLOSAPHILKVQORSISANQKRR 421
Qy      408  FSDQAGPAIPTNSYSKKTQSNNAENKRPEDDESGRKASST-----AKYPASPLPGL 461
      |||
Db      422  FSDHAGPSIPPAVSTYTRKPAQNSVESSEQKEWDQOTARILASTIVGSKSEVTASPLVGP 481
Qy      462  RKKTTPPTSTNSVLTSTNRSNPSPLERASTIGQASIONGKDS----- 504
      |||
Db      482  RKKSAGPS-NNVYSGGSMTRRNYYCERSTDRYALQNGRDSLTEMASASMSSTGTV 540
      |||
Qy      505  -----TAP-----QRPVVASPSAHNITSSGGA 526
      |||
Db      541  ASAGPSAPRROHOKSMSTSGHPIKYTLPTIKDSRQVAPRGTQVRVPAASPSAHSISAS--T 598
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QY	527	PDRTPPPGVSSRSFFHAGQLRQVDDOONLPGVTAPAPS----	CHSGCRGASGSITFSK	582
DB	559	PDRTFPPGGSSSRSTFHGBOL--RRRSAAVSCGPAPSDTALAALARRGSTGTGIISK	655	
QY	583	PTSKFRVRNLNLPESKDVEETLRPHVVGSGNDKEKEEFREAKPRLSLFTSMKTTSME	642	
DB	656	ITSKRVRRDPSGCGASGTDTR----GSSEPRDXCKEKGAKRSLRLFMTSMKTTSMD	711	
QY	643	PNEMMREIRKVLANDANSCSELHEKYMLCMHTGTEGHEDFVOMEWEVKLPRLSLNGVRFK	702	
DB	712	PNDWREIRKVLDAANTCDYEORERFLFCVHGDAQDSLVMEMEWCVCLPRLSLNGVRFK	771	
QY	703	RISGTSMAFKNIASKIANELKU 724		
DB	772	RISGTSIAFKNIASKIANELKU 793		
 RESULT 14 US-09-919-585-12 Sequence 12, Application US/09919585 Patent No. US3020115167A1 GENERAL INFORMATION: APPLICANT: Sun, Tian-Qiang APPLICANT: Feng, Jia-Jia APPLICANT: Reinhard, Christoph APPLICANT: Pantl, Wendy J. T. APPLICANT: Williams, Lewis T. TITLE OF INVENTION: ISOLATION OF DROSOPHILA AND HUMAN POLYNUCLEOTIDES ENCODING PAR-1 TITLE OF INVENTION: POLYPEPTIDES ENCODED BY THE POLYNUCLEOTIDES AND METHODS UTILIZING TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES FILE REFERENCE: PP-016093_002/200130_525 CURRENT APPLICATION NUMBER: US/09/919,585 CURRENT FILING DATE: 2001-07-30 NUMBER OF SEQ ID NOS: 22 SOFTWARE: FASTSEQ for Windows Version 4.0 SEQ ID NO 12 LENGTH: 795 TYPE: PRT ORGANISM: Homo sapiens US-09-919-585-12				
 Query Match 68.3%; Score 2552; DB 9; Length 795; Best Local Similarity 65.2%; Pred. No. 7,5e+148; Matches 525; Conservative 82; Mismatches 104; Indels 94; Gaps 16;				
QY	3	SARPTPLPLNRBDTQPPL--GHLD---	SKPSKSNMIRGNRSATSA-DEOPHIGNYR	54
DB	2	SARPTPLPVNERBDTENHTSVGDYTEPHIQPKSSSRQIIPRCRNISATSATDEQHIGNYR	61	
QY	55	LKLTIGKNFAKVLAARHLILTGKXVAVKIIDQTOLNSSLOKPREVRIMLVINHPNIVK	114	
DB	62	LQKITIGKNFAKVLAARHVLTGREVAVKIIDKTOLNPSTSLOKLPREVRIMKLNHPNIVK	121	
QY	115	LFEVLETETKIYLVMENVASGEVDYLYAHGRMKKEKARAFROVASAVQYCHOXKTVHR	174	
DB	122	LFEVLETETKIYLVMENVASGEVDYLYAHGRMKKEKARAFRIIVASAVQYCHOXKTVHR	181	
QY	175	DLKAEMLLLDDADNMIKIADFGFSNEFTGNLDTFCGSPPYAAPDLFOGXKYDGPEVDVV	234	
DB	182	DLKAEMLLLDDADNMIKIADFGFSNEFTGNLDTFCGSPPYAAPDLFOGXKYDGPEVDVV	241	
QY	235	SLGLVILYLVVSGSLPFDOQNKLREBRYLRGKRIIPFYMSSTDGCNLLKKFLILNPSRGST	294	
DB	242	SLGLVILYLVVSGSLPFDOQNKLREBRYLRGKRIIPFYMSSTDGCNLLKKFLILNPIKRGGS	301	
QY	295	LEQIMKORMNVVGHEDDELKPVEPLPDYKDPRTELNVSNGYTREBIODSLVGQRVNEV	354	
DB	302	LEQIMKORMNVVGHEDDELKPVEBDDPDFNTDKIDINVTMGFARDEINDALLNQKYDEV	361	
QY	355	MATVILLIGKYSSELEG-----DTITLKPRRSADULTNSAPSPSH-KVQNSVSANPQKR	407	
DB	362	MATVILLIGRKPRPEEGGESSLSGNICONSRRSSDNLNSTQSAPHLVQORSISANOQR	421	

QY	408	FSDDQGPALPFSNNSISKTQSNNAENKPRPE--DRESGRASST---- <td>461</td>	461
Db	422	FSDAHGPSTLPPVASYTKRBPQANSVSEBQKEBWDKVARKLGSITTVGSKSEMTASPLVGP	481
QY	462	RKTTPTSTNSVLSTSTNRSRNSPLLEPASLGGQASLONKQDS-----	504
Db	462	RKGSSTIPS--NNVSGSGSWARNRTVTCERTTORIYVALONGKSSSLTMSVSSISSAGSV	540
QY	505	-----TAP-----	526
Db	541	ASAVSAPRPHQKSMSTSGHPFKVTLPTIKDQSEAVRPETTORVPAPASASHSISRA--T	598
QY	527	PDRTNPPGVSRSRSTFHAGQLFQVRDQNLPGVTPPASGSGSQ-----RCGASGIS	581
Db	599	PDRTFPPGSSRSRSTFHGQL--RERSVAVNGPASPSS--HETGAPAHARRCTSGIIS	654
QY	582	KFTSFVVRNINPEPSKQXVERTLRPHVVGSGGNDKE--KEEPREAKPRSLPTWSKTT	639
Db	655	KITSFVVRNDSEGGASGRTDTSR---STSEPPERDDEBGGDSKPRSLRFTWSKTT	710
QY	640	SMEPNEMRERIRKVLVDANSQSELHEKXWLLCMHGTPGHEDPVQWEMEMECUKLPRLSLV	699
Db	711	SMDPRDMMREIRKVLVDANNQDQEQERFLPLFCVHDARDQSLVQWEMEMECUKLPRLSLV	770
QY	700	RPKRISGTSMAPKNIASKIANELKL	724
Db	771	RPKRISGTISIAFKNIASKIANELKL	795

; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
; 60/228,056
; PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-0
; 25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 795
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023242A1 7473244CD1
US-10-311-034-4

Query Match 68.3%; Score 2552; DB 15; Length 795;
Best Local Similarity 65.2%; Pred. No. 7.5e-148;
Matches 525; Conservative 82; Mismatches 104; Indels 94; Gaps 16;

QY 3 SARTPLPTLNERDETOPTL--GHLD-----SKPSKSNMTRGRNSATSA-DEOPHIGNR 54
DB 2 SARTPLPTLNERDETOPTL--GHLD-----SKPSKSNMTRGRNSATSA-DEOPHIGNR 61
QY 55 LKTIIGKNPAKYLAARHILTGKEVAVKIDKTQLNSSLQKLFREVRIMKVLNHPNIVK 114
DB 62 LQTIIGKNPAKYLAARHILTGKEVAVKIDKTQLNSSLQKLFREVRIMKVLNHPNIVK 121
QY 115 LFEVIEKTEKLYLMEYASGGEVVDYLAHGRMKEKARAKFRQVSAVOYCHQKTIVHR 174
DB 122 LFEVIEKTEKLYLMEYASGGEVVDYLAHGRMKEKARAKFRQVSAVOYCHQKTIVHR 181
QY 175 DLKAEMLLDADNMIKADFGFSENEFTFGKLDTPCGSPRYAAPLFOGKYVDGPEVDW 234
DB 182 DLKAEMLLDADNMIKADFGFSENEFTFGKLDTPCGSPRYAAPLFOGKYVDGPEVDW 241
QY 235 SLGVIIYTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKFLIINPSKRG 294
DB 242 SLGVIIYTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKFLIINPSKRG 301
QY 295 LEOIMKDRMNVGHEDELKPYVEPLDYPKDPRTTELWVMGTYREBIODSLVGQRYNEV 354
DB 302 LEOIMKDRMNVGHEDELKPYVEPLDYPKDPRTTELWVMGTYREBIODSLVGQRYNEV 361
QY 355 MATYLLGYSSLEG-----DTITLKPRPSADLTNNSAPSPSH--KVQSVANPKQRR 407
DB 362 MATYLLGYSSLEG-----DTITLKPRPSADLTNNSAPSPSH--KVQSVANPKQRR 421
QY 408 FSDQAGPALPTSNYSKKTQSNNAENKRPPE--DRESGRKASST-----AKVPASPLPGL 461
DB 422 FSDHAGBSIPPAVSYTKRPQANVESBQKEHMDKDVARKLGITTVGSKSEMTASPLVGP 481
QY 462 RKTTTPTSTNYSVLSTNRSRNSPLIERASLGQASIQNGKDS-----504
DB 482 RKTSSTIPS--NNYSGGSMARNTYCEFTTDRYVALQNGKDSLTMSVSSISSAGSSV 540
QY 505 -----TAP-----CRVPVAPSAHNISSSGGA 526
DB 541 ASAVPSPAPRHQKSMSTSGHPIKVTLPTIKDQSEAYRPGTTQKVPAPSAHISTA--T 598
QY 527 PDRTPNPRGVSSNSTFHAGQLROVDOQLPYGVTPASPSSGHSQG-----RQASGSIFS 581
DB 599 PDRTPNPRGVSSNSTFHAGQLROVDOQLPYGVTPASPSSGHSQG-----RQASGSIFS 654
QY 582 KPTSKFVRRLNLPESKDVETLRPHVVGSGGNDKE--KEEPRKAPRSIRFTWSMKTT 639
DB 655 KITSKFEVRDPSGEGASGRDTSR-----STSGEPKEREKESKPRSLRFTWSMKTT 710
QY 640 SMEPNEMREIRVULANSQSELHEKMYMLCMHGTPGHEDFVQWEMEVCKLPRLSLNGV 699
DB 711 SHDPNDMEIRVULANSQSELHEKMYMLCMHGTPGHEDFVQWEMEVCKLPRLSLNGV 770
QY 700 RFRKISGTSMAPKNIAKIANELKL 724

DB 771 RFRKISGTSMAPKNIAKIANELKL 795

Search completed: February 26, 2005, 18:03:59
Job time : 142 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 17:42:42 ; Search time 44 Seconds
(without alignments)
1583.203 Million cell updates/sec

Title: US-10-760-407-2

Perfect score: 3737

Sequence: 1 MSASRTPLPLTNEDEQPT.....SGTSMARKNIASKIANELKL 724

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3515	94.1	745	2 G01025	serine/threonine p
2	3467	92.8	774	2 I48609	probable serine/th
3	2381	63.7	713	2 S27966	probable serine/th
4	1771.5	47.4	1192	2 T18611	probable serine/th
5	1707	45.7	1246	2 G89287	protein H39E23.1 l
6	988.5	26.5	1398	2 T13741	hypothetical prote
7	981	26.3	798	2 JC7500	gik protein - chic
8	928	24.8	481	2 I49072	protein kinase - m
9	821.5	22.0	891	2 T40503	protein kinase kin
10	812.5	21.7	891	2 A38903	protein kinase 1 -
11	797.5	21.3	633	1 A26030	serine/threonine-s
12	778.5	20.8	887	2 T20941	hypothetical prote
13	776.5	20.8	651	2 S52244	p95B93 protein - A
14	775	20.3	602	2 S72513	FG2 protein - yea
15	757.5	20.3	512	2 T52633	serine/threonine-s
16	752.5	20.1	504	2 T07415	probable serine/th
17	745.5	19.9	512	1 T01446	serine/threonine-s
18	744	19.9	504	2 T10449	probable serine/th
19	740	19.8	746	2 S62365	SNF1-related prote
20	727.5	19.5	511	1 A56009	serine/threonine-s
21	716.5	19.2	576	2 T41587	probable carbon ca
22	710.5	19.0	512	2 T07788	serine/threonine-s
23	710.5	19.0	513	1 S60303	serine/threonine-s
24	708.5	19.0	726	2 T33998	hypothetical prote
25	707.5	18.9	473	1 S59941	serine/threonine-s
26	707.5	18.9	1558	2 T29253	hypothetical prote
27	707	18.9	552	1 S51025	hydroxymethylglut
28	705.5	18.9	552	1 A53621	hydroxymethylglut
29	699	18.7	562	2 T29858	hypothetical prote

30	690.5	18.5	1016	2 T25433	hypothetical prote
31	688.5	18.4	513	1 S60304	serine/threonine-s
32	687.5	18.4	472	2 B90100	SNF-related kinase
33	687.5	18.4	510	2 T04145	serine/threonine p
34	681	18.2	1064	2 S52687	serine/threonine-s
35	679	18.2	502	1 A41361	serine/threonine-s
36	661.5	17.7	1518	2 S37928	probable purine nu
37	650.5	17.4	1147	2 S64930	serine/threonine-s
38	641.5	17.2	1142	2 S59359	G1N4 protein - yea
39	638	17.1	622	1 S44859	serine/threonine-s
40	634	17.0	915	2 S74283	probable protein k
41	633	16.9	480	2 A86427	probable serine/th
42	632.5	16.9	440	2 T14736	probable serine/th
43	624.5	16.7	489	2 T04862	probable serine/th
44	619	16.6	334	2 T22427	hypothetical prote
45	615.5	16.5	440	2 T14735	probable serine/th

ALIGNMENTS

RESULT 1

G01025

serine/threonine protein kinase - human

C:Species: Homo sapiens (man)

C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 16-Aug-2004

C/Accession: G01025

R/Navarro, E.

submitted to the EMBL Data Library, April 1996

A/Reference number: H00564

A/Accession: G01025

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-745 <NAN>

A/Cross-references: UNIPROT:Q15524; UNIPROT:Q96H3; EMBL:X97630; NID:g1310674

F:Superfamily: protein kinase homology

F:18-271/Domain: protein kinase homology <KIN>

Query Match 94.1%; Score 3515; DB 2; Length 745;

Best Local Similarity 92.3%; Pred. No. 7.6e-125;

Matches 688; Conservative 1; Mismatches 2; Indels 54; Gaps 1;

QY	34	MIRGRNSATSADROPHIGNRLIKTIGKGFAYKLABHILTKQVAVKIIDTQUNSSS	93
DB	1	MIRGRNSATSADROPHIGNRLIKTIGKGFAYKLABHILTKQVAVKIIDTQUNSSS	60
QY	94	LQKLPEVRIMKYNPNIVKLFVILETEKTLILVMEYASGSEVFDLVHGMKEKEAR	153
DB	61	LQKLPEVRIMKYNPNIVKLFVILETEKTLILVMEYASGSEVFDLVHGMKEKEAR	120
QY	154	AKRQVSAVQYCHQKFIYHARDIKAEMLLDADMNIKIADFGSNEFTFGNKLDTPCGSP	213
DB	121	AKRQIVSAVQYCHQKFIYHARDIKAEMLLDADMNIKIADFGSNEFTFGNKLDTPCGSP	180
QY	214	PYAPPELPGKKKVDGPEVDWISGLVILYTVSSSLPDDGNLKELEERYLRGKVRAPFYM	273
DB	181	PYAPPELPGKKKVDGPEVDWISGLVILYTVSSSLPDDGNLKELEERYLRGKVRAPFYM	240
QY	274	STDCENILKKFLLINPSKGTLLIQIMKDRMANYGHEDDELKPYVEPLPDVKDPRRTLEW	333
DB	241	STDCENILKKFLLINPSKGTLLIQIMKDRMANYGHEDDELKPYVEPLPDVKDPRRTLEW	300
QY	334	SMGYTRREIIDSIVGGRYNEVMATYLLGYKSSLEGGDTTLTKRPSADI TNSASAPSH	353
DB	301	SMGYTRREIIDSIVGGRYNEVMATYLLGYKSSLEGGDTTLTKRPSADI TNSASAPSH	360
QY	394	KVGRSVSANPKORRFSDDGAPALPTNSYSKKTKQSNNAEKREEDRESGRKASSTAKVP	453
DB	361	KVGRSVSANPKORRFSDDGAPALPTNSYSKKTKQSNNAEKREEDRESGRKASSTAKVP	420
QY	454	ASPLPGLERKKTPTPTSTNSVLSTSTNRSHNSPLLRASLGGASIONGKX-----	503
DB	421	ASPLPGLERKKTPTPTSTNSVLSTSTNRSHNSPLLRASLGGASIONGKXSLTMPGRAS	480

QY 504 -----STAPORVPVASPAHN 519
DB 481 TASASAGVSAARPROHOKSMGSHVHPKASGLPTESNCEVPBSTAPORVPVASPAHN 540
QY 520 ISSSGAPADRTNPRGVSSRSTFHAQGLROYRDOQNLPGVTPASPAGSHGSGRRGASGI 579
DB 541 ISSSGAPADRTNPRGVSSRSTFHAQGLROYRDOQNLPGVTPASPAGSHGSGRRGASGI 600
QY 580 FSKTSTKFRVRNINPEPSKQVETILRPHVVGSGNDKEKEFRBAKPRSLRFTWSMKTTS 639
DB 601 FSKTSTKFRVRNINPEPSKQVETILRPHVVGSGNDKEKEFRBAKPRSLRFTWSMKTTS 660
QY 640 SMEENEMREIRKVLDAANSQSEIHEKYMILCMHGTGCHDFVQWEMEVCKLRLSLANGV 699
DB 661 SMEENEMREIRKVLDAANSQSEIHEKYMILCMHGTGCHDFVQWEMEVCKLRLSLANGV 720
QY 700 RFKRISGTSMAFKNIASKIANELKL 724
DB 721 RFKRISGTSMAFKNIASKIANELKL 745

RESULT 2

148609
probable serine/threonine-specific protein kinase (EC 2.7.1.1) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Aug-2004
C/Accession: I48609; S31333
R/Inglis, J.D.; Lee, M.; Hill, R.E.
Mamm. Genome 4, 401-403, 1993
A/Title: Emk, a protein kinase with homologs in yeast maps to mouse chromosome 19.
A/Reference number: I48609; MUID:93364122; PMID:8358177
A/Accession: I48609
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-774 <ING1>
A/Cross-references: UNIPROT:Q05512; EMBL:X70764; NID:957919; PIDN:CAAS0040.1; PID:957920
R/Inglis, J.D.; Lee, M.; Hill, R.E.
submitted to the EMBL Data Library, January 1993
A/Description: A novel protein kinase with homologues in yeast maps to mouse chromosome
A/Reference number: S31333
A/Molecule type: mRNA
A/Residues: 1-698; 'K', 700-702, 'GRGLPTAAKASCTSGTCYCAQMAHQATRR', 731-774 <ING2>
A/Cross-references: EMBL:X70764
A/Genes: emk
C/Superfamily: protein kinase homology
C/Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F/51-304/Domain: protein kinase homology <KIN>
F/59-67/Region: protein kinase ATP-binding motif

Query Match 92.8%; Score 3467; DB 2; Length 774;
Best Local Similarity 88.3%; Pred. No. 4.9e-123;
Matches 687; Conservative 11; Mismatches 22; Indels 58; Gaps 3;

QY 1 MSASRTPLPTLNDRDTEOPLTGLHDSKPSKSMNIRGMSAATSADOPHIGNVRLIKTIG 60
DB 1 MSASRTPLPTLNDRDTEOPLTGLHDSKPSKSMNIRGMSAATSADOPHIGNVRLIKTIG 60
QY 61 KGNFAVKLARHILTGKEVAVKIIDKTQNLSSSLQKLFREVRIMKLNHPNIVKLFVIE 120
DB 61 KGNFAVKLARHILTGKEVAVKIIDKTQNLSSSLQKLFREVRIMKLNHPNIVKLFVIE 120
QY 121 TEKTLILVMEYASGGEVDYLVAHGMRKEKARAKRROVSAVOYCHQKFIYHRDLKAE 180
DB 121 TEKTLILVMEYASGGEVDYLVAHGMRKEKARAKRROVSAVOYCHQKFIYHRDLKAE 180
QY 181 LLLDADNMIKIADFGSNEFTFGNKLDTFGSGSPYAAPLFGSKKYDGEVDVWSLGL 240
DB 181 LLLDADNMIKIADFGSNEFTFGNKLDTFGSGSPYAAPLFGSKKYDGEVDVWSLGL 240
QY 241 YTLVSGSLPFDGQNLKELEERVLRGKRYIPFYWSTDCENILKKFLILNPSKRGTLLEQIMK 300

DB 241 YTLVSGSLPFDGQNLKELEERVLRGKRYIPFYWSTDCENILKKFLILNPSKRGTLLEQIMK 300
QY 301 DRWMNVGHEDDELKPYVEPLPYKDPRTIELVWSMGYTFEEIIDSIVGQRYNEVATYLL 360
DB 301 DRWMNVGHEDDELKPYVEPLPYKDPRTIELVWSMGYTFEEIIDSIVGQRYNEVATYLL 358
QY 361 LGYKSELLEGDTITLKPESADLTNSAPSPSHKVQSVSANPKQRFSDQGAIPTSN 420
DB 359 LGYKSELLEGDTITLKPESADLTNSAPSPSHKVQSVSANPKQRFSDQGAIPTSN 418
QY 421 SYSKTQSNANNAKKPEERRESGRKASSTAKVAPLGLFEKTKTPPTSTVSTSTN 480
DB 419 SYSKTQSNANNAKKPEERRESGRKASSTAKVAPLGLFEKTKTPPTSTVSTSTN 476
QY 481 RSRNSPLERASLQASLQNGKD----- 503
DB 477 RSRNSPLERASLQASLQNGKSLTMPGSRASTASAAVSAARPROHOKSMGSHVHPN 536
QY 504 -----STAPORVPVASPAHNISSSGAPDRINPRGVSSRSTFHAQ 546
DB 537 KASGLPTESNCEVPBSTAPORVPVASPAHNISSSGAPDRINPRGVSSRSTFHAQ 596
QY 547 LRQVRDQNLPGVTPASPAGSHGSGRRGASGISFESKTSKFRVRLNPESKDRVETLRP 606
DB 597 LRQVRDQNLPGVTPASPAGSHGSGRRGASGISFESKTSKFRVRLNPESKDRVETLRP 656
QY 607 HVVGSQNDKEKEFRBAKPRSLRFTWSMKTTSMEENEMREIRKVLDAANSQSEIHEK 666
DB 657 HVVGSQNDKEKEFRBAKPRSLRFTWSMKTTSMEENEMREIRKVLDAANSQSEIHEK 716
QY 667 YMLLCVHGTGCHDFVQWEMEVCKLRLSLANGVRRKRIISGTSMAFKNIASKIANELKL 724
DB 717 YMLLCVHGTGCHDFVQWEMEVCKLRLSLANGVRRKRIISGTSMAFKNIASKIANELKL 774

RESULT 3

S27966
probable serine/threonine-specific protein kinase (EC 2.7.1.1) - human
N/Alternate names: protein p78
C/Species: Homo sapiens (man)
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
R/Maheshwari, K.K.; Som, S.; Parsa, I.
submitted to the EMBL Data Library, January 1992
A/Description: Sequence of a cDNA encoding 78kD marker protein lost in chemically induce
A/Reference number: S27966
A/Accession: S27966
A/Molecule type: mRNA
A/Residues: 1-713 <MAH>
A/Cross-references: UNIPROT:P27448; EMBL:M80359; NID:9189511; PIDN:AAAS9991.1; PID:91895
C/Superfamily: protein kinase homology
C/Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F/54-307/Domain: protein kinase homology <KIN>
F/62-70/Region: protein kinase ATP-binding motif

Query Match 63.7%; Score 2381; DB 2; Length 713;
Best Local Similarity 66.2%; Pred. No. 1.8e-82;
Matches 498; Conservative 75; Mismatches 109; Indels 70; Gaps 18;

QY 3 SARTEPLPTLNDRDTEOPLTGLHDSKPSKSMNIRGMSAATSADOPHIGNVRLIKTIG 57
DB 2 STRTEPLPTLNDRDTEOPLTGLHDSKPSKSMNIRGMSAATSADOPHIGNVRLIKTIG 60
QY 58 TIGKGNFAVKLARHILTGKEVAVKIIDKTQNLSSSLQKLFREVRIMKLNHPNIVKLF 117
DB 61 TIGKGNFAVKLARHILTGKEVAVKIIDKTQNLSSSLQKLFREVRIMKLNHPNIVKLF 120
QY 118 VIEFEKTLILVMEYASGGEVDYLVAHGMRKEKARAKRROVSAVOYCHQKFIYHRDLK 177
DB 121 VIEFEKTLILVMEYASGGEVDYLVAHGMRKEKARAKRROVSAVOYCHQKFIYHRDLK 180
QY 178 AENLLDADNMIKIADFGSNEFTFGNKLDTFGSGSPYAAPLFGSKKYDGEVDVWSLGL 237

Db 181 AENLLADAMNLIKADFGSNEFTVGGKLDITFCGSPFYAAPELFGKKGTPEDVWSLG 240
Qy 238 VILYTVVSGSLPFDGQNLKELREYVLRGKTRIPFYMSTDCBNLIKFLINPSKRGTLQ 297
Db 241 VILYTVVSGSLPFDGQNLKELREYVLRGKTRIPFYMSTDCBNLIKFLINPSKRGTLQ 300
Qy 298 IMKDRMNVGHDEDELKVEYEPPLPDYDPRTELVMGMVTRREIDSLVGQRNEMAT 357
Db 301 IMKDRMNVGHDEDELKVEYEPPLDSDQKRIDVMGMVYQSEIQSLSKMKYDEITAT 360
Qy 358 YLLLGKSELEGGDTITLKRPSPADLTNSAPSPSHKVRQSVSANPFQRFSDOAGPAIP 417
Db 361 YLLLGKSSSEV-----RPSDDLNTSGQSPHHKVRQSVSSQKQRKYSDBAGGPIR 411
Qy 418 TNSYSKKTQSNNAENKRPEDRESGRKASTAK---VPASPLPG-----LER 462
Db 412 SYVAAPKRSQSTVSDPL-KEDGISRKSQSAVGKGIAPASPMGNANPNKADIPER 470
Qy 463 KKTTPPSTNSVLTSTNRSRNPRLERASLGQAS-IQNGKD-STAP-QRPVPAAPSAN 519
Db 471 KKSSTVPSSTVAGGMRNR-TYVCSERITDDRHSVLQNGKENSITPDQRTVA--STHS 527
Qy 520 ISSSGAPDRTPNPRGVSSRSTFHAQQLRQVRDQNLPGVTAPSPS-GH-----SQGR 573
Db 528 ISSA-ATPDRIRPRGTASTFTHG---QPRERRTATYNGPRAPSPSLSHSATPLSGTRS 582
Qy 574 GAGSIFSKFTSKFVR-RNINPEBSKQDVETLAPHVVGSGANDKEKEEPKAKRSIRFT 632
Db 583 RGSITTLFSKLTSLKTRSRNVSA-----KQKDNKEAKPRSRIRFT 621
Qy 633 WSKHTTSMENPMNRIRRYLDANSQSELEHKYMLCMHGTPGHEDPFWOMEVCKLP 632
Db 622 WSKHTTSMENPMNRIRRYLDANNCDYQREKFLFVGHGDAENLQVMEVECKLP 681
Qy 693 RLSLNGVRFKRISGTSMAFKNIASKIANEKL 724
Db 682 RLSLNGVRFKRISGTSIAFKNIASKIANEKL 713

RESULT 4
T18611
Probable serine/threonine-specific protein kinase (EC 2.7.1.-), long splice form - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T18611; T18610; T23144; T23143
R/McMurray, A.
Submitted to the EMBL Data Library, October 1996
A/Reference number: Z18997
A/Accession: T18611
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1192 <W1L4>
A/Cross-references: UNIPROT:Q9TW45; EMBL:Z81027; P1DN:CAB54179.1; GSPDB:GN00023; CESP:H3
A/Experimental source: clone AH10
A/Experimental source: clone AH10
A/Accession: T18610
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-487,536-1192 <W1L2>
A/Cross-references: EMBL:Z81027; P1DN:CAB54178.1; GSPDB:GN00023; CESP:H39E23.1b
A/Experimental source: clone AH10
R/McMurray, A.
Submitted to the EMBL Data Library, June 1997
A/Reference number: Z19696
A/Accession: T23144
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1192 <W1L3>
A/Cross-references: EMBL:Z96102; P1DN:CAB54263.1; GSPDB:GN00023; CESP:H39E23.1a
A/Experimental source: clone H39E23
A/Accession: T23143
A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA
A/Residues: 1-487,536-1192 <W1L4>
A/Cross-references: EMBL:Z86102; P1DN:CAB54262.1; GSPDB:GN00023; CESP:H39E23.1b
A/Experimental source: clone H39E23
C/Genetics:
A/Map position: 5
A/Intons: 10/3; 33/3; 67/3; 139/2; 183/3; 451/3; 487/3; 535/3; 631/1; 825/2; 914/3; 99
C/Keywords: alternative splicing; ATP; phosphotransferase; serine/threonine-specific pr
F;1-1192/Product: probable serine/threonine-specific protein kinase, long splice form #
F;1-487,536-1192/Product: probable serine/threonine-specific protein kinase, short sp11

Query Match 47.4%; Score 1771.5; DB 2; Length 1192;
Best local Similarity 39.0%; Pred. No. 1.8e-59;
Matches 423; Conservative 106; Mismatches 179; Indels 377; Gaps 25;

Qy 2 SSARPLPLNERDTEQPTLGHLD--KSSKSNMIRGRNATSADQPIGNYRLTKTI 59
Db 123 SSAR-----YSSGSRHPTSGSSSHARSQSGM-SSRGAARNDDQDVHGVKYLTKTI 176
Qy 60 GKGNPAKVKLARIILKGVAVVNIIDKQLNSSLQKLPREVRIKVLNPNVYKLPYI 119
Db 177 GKGNPAKVKLAKVITGHEVAIKIIDKTLNPSLQKLPREVRIKVLNPNVYKLVQVM 236
Qy 120 ETEKTLVLMVEYASGGEVFDYLAHGRMKEKARAKFRQVSAVOYCHQKFIYHRLKAE 179
Db 237 ETEQTLVLEIYASGGEVFDYLAHGRMKEKARAKFRQVSAVOYHLSNIIHRLKAE 236
Qy 180 NLLLDAMNLIKADFGSNEFTFGKLDITFCGSPFYAAPELFGKKGTYDGEVDVWSLGI 239
Db 297 NLLLDAMNLIKADFGSNTFTSLGNKLDITFCGSPFYAAPELFGKKGTYDGEVDVWSLGI 356
Qy 240 LYTIVSGSLPFDGQNLKELREYVLRGKTRIPFYMSTDCBNLIKFLINPSKRGTLQ 239
Db 357 LYTIVSGSLPFDGQNLKELREYVLRGKTRIPFYMSTDCBNLIKFLINPSKRGTLQ 416
Qy 300 KDRMNVGHDEDELKVEYEPPLPDYDPRTELVMGMVTRREIDSLVGQRNEMAT 356
Db 417 KDRMNVGHDEDELKVEYEPPLPDYDPRTELVMGMVTRREIDSLVGQRNEMAT 476
Qy 357 TYLLGKSELEGGDTITLK----- 376
Db 477 TYLLGKSELEGGDTITLK----- 536
Qy 377 ---PRPSADIT-----NSAPSP----- 390
Db 537 SRYRSASATATGASITAGSALSAANAOKHQSSAPSSGSSSSRRSQNDAAATAGCT 536
Qy 391 -----PSHKVQRSVS----- 400
Db 597 VVNSGTRHGGVQNRAPTSRQATISLLQPSYSPSSNTTQIAQIPPLFNENSTATSSAQ 656
Qy 401 -----ANPK----- 411
Db 657 PSTGITGTRKLIADPKRIRPLNSTAVGNGHRTATGAVANNGGISHRDHAGQOQVNLGTS 716
Qy 412 -----AGPAITPSNSYSKKTOS----- 432
Db 717 STWMSKILNKTPAAGCTAATSSSSSSSASTABLRQSGSQISHAPTEPVREDDEENSE 776
Qy 433 NKR-----PEEDRESG-----RKXSSAPKAPASPLPLGERKKT 466
Db 777 NQNGNVPLIGVGVPQTSFAVQVTEBATSSDKQOQKASS--ETPKSKPSMIIHSPS 834
Qy 467 PTPS----- 474
Db 835 MPSPQMMTAMESLKLSESGQTGGPTVATGGPPQQRATSSQMSRATNTNSAMGASGGAA 894
Qy 475 LSTSTSRKNSPLLEPASLGQASIQ-----NGKSTAPQV 510
Db 895 AASATQNLGAP---SSTGASQOYHPRKAPSSSSSSSTNPRHQQLTHNAPSFTVPSY 950
Qy 511 PVASPSAHNISSG--GAPDRTPNPRGVSSRSTFHAQQLRQV--DQQLNPGVVTAPSPS 566

Db 951 QIPSTAVNTVSTGMPSSSSSAFPRNTRKQTH-GKTEKDKGDDSSPEIGETPGNVS 1009
Qy 567 GHSQG--RRGASGSIFFSKTFSKYVRNLNBPESKDRVETLLRPHVVGSGGNDKEKEFR-- 622
Db 1010 IGATGPGSANNAAEATYWSKL-SKLTRRDHNR-ESMTQPVSGAGCTIGASQCGQTAAALAI 1067
Qy 623 -----BAKPRSLRFTWMSMTTSSMENEMMERIRKYLDAVNSC 659
Db 1068 REOSGPIAPGAGVAPSLPIHESGVKPRSLRFTWMSMTTSSLAEDDMREIRKYLDAVNSC 1127
Qy 660 QSEIHEKYMILCMHGTGHEDEPVQWEMEVCKLPRLSLNGVRFKRISGTSMAFKNIASKIA 719
Db 1128 DYERKERYMILCVHGDVNTSLVQWEMEVCKLPRLSLNGVRFKRISGTSIGFKNIASKIA 1187
Qy 720 NELKL 724
Db 1188 QELNLT 1192

RESULT 5

G89287
Protein H39E23.1 (imported) - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C/Accession: G89287
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A/Reference number: A75000; MUID:99069613; PMID:9851916
A/Note: see webstiles genome.wustl.edu/gen/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A/Accession: G89287
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1246 <STO>
A/Cross-references: GB:chr_V; PIDN:CAB09532.1; PID:g3878100; GSPDB:GN00023; CESP:H39E23.
C/Genetics:
A/Gene: H39E23.1
A/Map position: 5

Query Match 45.7%; Score 1707; DB 2; Length 1246;
Best Local Similarity 34.1%; Pred. No. 5e-57;
Matches 420; Conservative 113; Mismatches 174; Indels 524; Gaps 24;
Qy 15 DTBQPTLGHLDSPSSKSMIRGNKATSA---DEOPHIGNYRLTLTGKGNFAKYKLAR 71
Db 19 DGDVTHNRKSSSSHAASSTGQSGMSSRSARNDQVHVGKYLTLTIGKGNFAKYKLAK 78
Qy 72 HILTGKEVAVKIIDKTQNLNSSLQKLFREVRIMKVLNHPNIVKLFEVIEKTEKLYLWMEY 131
Db 79 HVTGHEVAIKIIDKTALNSSLQKLFREVRIMKVLNHPNIVKLFEVIEKTEKLYLWMEY 138
Qy 132 ASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYCHQKPLVHRDLKAENLLDADANNIKI 191
Db 139 ASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYCHQKPLVHRDLKAENLLDADANNIKI 198
Qy 192 ADGFGNEFTFGKLTDFGSSPPYAAPBLFQGGKYTGPERDVWSLGVILYTLVSGSLPDP 251
Db 199 ADGFGNFTSLGKLTDFGSSPPYAAPBLFSGGKYTGPERDVWSLGVILYTLVSGSLPDP 258
Qy 252 GQNLKELREVLKGYRIPFYMSITDCEMLIKFLINPSKRGTLBEQIMKDRMNVGHEDD 311
Db 259 GQNLKELREVLKGYRIPFYMSITDCEMLIKFLINPSKRGTLBEQIMKDRMNVGHEDD 318
Qy 312 ELKPYEPLPDYKDPRTBLMV---SMGYTRBIEIDSLVQRYNEVATYLLGYKSSSL 368
Db 319 ELKPYEPLPDYKDEQRIEKLQIFQGFYKAILLESVEKEKEDIHATYLLGKSKDM 378
Qy 369 EGGTTLK-----PPSADLT- 384
Db 379 DASEITMAOGLSHSSINWSSLGHPAGVITREHTSSASGSSASPSRYSRSSATATG 438

Qy 385 -----NSSAB----- 390
Db 439 ASITGASALASANNOKHOSSAABSGSSSSSRSSQNDAAATAGGVVMSGTRHGVQ 498
Qy 391 -----PSHKVQRVS-----A 401
Db 499 MRAQPTSRQATISLQPPSKSSNTQTQIAQIPLFNRSSTATSSAAQSTGITGRKIA 558
Qy 402 NPK-----QRPSDQ----- 411
Db 559 DPKGRIPILNSTAVQGHRTATGAVAANNNGIPSHRDHAQQQYMNQLTSITMMSKLINKTP 618
Qy 412 -AGPAIPTSNSYSKTKQS-----NNAEKR----- 435
Db 619 AAGGTAATSSSSSSATSTAPLQKSGSQISHAPTEPVIREDDENNENGNVPLIGGV 678
Qy 436 -----PEEDREG-----RKASSTAKVPAPL----- 457
Db 679 GPOTSPAVQVPTEDATSSSDKXQQQKASSETPKESNPIVMQNMLNLSKSLDSSAAT 738
Qy 458 -----PGLERKKTPT----- 468
Db 739 SYETPRRPFIAGRSEPSATPRRRHQTVVDARHLQTPDTPRYHEDTLLDRQMBAL 798
Qy 469 -----PSINSVL-----TSNRSRN-----SPLER 490
Db 799 YVSTASRMTGVLPTPTSNSTSSSFLVEPLTHVAASPDITTTPTKSVTTSPPYERR 858
Qy 491 ----- 490
Db 859 TSPFPMVLIVLLCDNGLRMPMSMHQSPMPSPQMTAMBSLKLSGSGQTGPTVATGG 918
Qy 491 -----ASLGAS----- 497
Db 919 PQORATSQGMSRATTNASGASGGAATAATNOLSGAPSSYGASSQYHPAPSSS 978
Qy 498 -----IQNGKDSPTAPQRPVAPSPAHNISSG--GAPDRNFPRGVSRSTP 542
Db 979 SSSSTNPHQOLTHNASFSTVPSYQIPTSTAVNTSTGMPSSSSSAFPRNTRKQTH 1038
Qy 543 HAGQLRQVR--DOQLPYGVTPASPSPGSGQ--RRGASGISFKSTKSVFRNLNBPSSK 598
Db 1039 H-GKTEKDKGDDSDDEIGETPGNVISGATGPGSANNAAEATYWSKL-SKLTRRDHNR-BSM 1095
Qy 599 DRYETLRPHVVGSGGNDKEKEFR-----EAKPRSLRFTW 633
Db 1096 TQPVSGRAGTIGASQCGQTAAALAIHQSGPIAPGAGVAPSLPIHESGVKPRSLRFTW 1155
Qy 634 SMKTTSMENPMMEIRKVLDAVNSQSEIHEKYMILCMHGTGHEDEPVQWEMEVCKLP 693
Db 1156 SMKTTSSLAIPDDMMERIKVLDANGCDYERBRVITLCVHGDPNTSLVQWEMEVCKLP 1215
Qy 694 LSLNGVRFKRISGTSMAFKNIASKIANELKL 724
Db 1216 LSLNGVRFKRISGTSIGFKNIASKIAQELNLT 1246

RESULT 6

T13741
hypothetical protein 22E5.8 - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C/Accession: T13741
R:Murphy, L.; Harris, D.; Barrell, B.
submitted to the EMBL Data Library, April 1999
A/Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A/Reference number: Z17668
A/Accession: T13741
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1398 <MOR>
A/Cross-references: UNIPROT:O77268; EMBL:AL031765; NID:e1371523; PID:e1329905; PIDN:CAA2
C/Genetics:

A/Cross-reference: FlyBase:FBgn000667
A/Intons: 205/3; 227/1; 322/3; 688/3; 782/3; 814/2; 1363/3
A/Note: EG:22E5.8

Query Match 26.5%; Score 988.5; DB 2; Length 1398;
Best Local Similarity 35.1%; Pred. No. 4.1e-30;
Matches 266; Conservative 99; Mismatches 230; Indels 163; Gaps 20;

```
QY 28 PSSKSNMIRGRNATSD-----EQPHIGNRLKTKTGKGFPAVKLARHLTGKEVAVK 82
DB 112 PSPSSAV-GAGGISGDLKLEKPMRVGFDIRTTGKGFPAVKLARHLTGKEVAIK 170
QY 83 IIDKTQLNSSLQKLFREVRIMKVLNHPNIVKLFVETETKTYLWMEYASGGEVFDYLV 142
DB 171 IIDSGQDQNTLQKVEVEIMKRLKPHIILKYQWETKMITYEYASGGEIFDYIA 230
QY 143 AHGMEKEAKAFKQVAVQCHQKFIYHRDIKAENLLLDADMTKIADFGFSNEFTF 202
DB 231 KYGMSBSAARFKWQIISAVEYCHKKGIYHRDLKAENLLLDLNMNIKIADFGFSNFKP 290
QY 203 GNLDTFCGSPRYAPRLFOGKATDGEVDVWISGLVLLTYVSGSLFPDQNLKELREY 262
DB 291 GBLATWCGSPRYAAPRVFEGKQYTGPEIDWISGLVLLYVCGALFPDSTLQSLRDY 350
QY 263 LRGRYRIPYMWSTDCENLKKKFLINPSKGTLEQIMKDRM-----NYGHE 309
DB 351 LSGRFRIPFMSSECEHLIRMLVLEPTRTTIDQIGHKMCHELLEHVLAKYNG-- 408
QY 310 DBELKPYVEPLPDYKDRTELWVS-MGYTREIQLDSLVGQRYNEVATYLLLGKSSSEL 368
DB 409 -AERQTSVEPSEDI-----LRIMAEYVIGSDKTRASLKNQTYDHAIVYLL----- 455
QY 369 EDQITTLKPRPADLNTS---SAPSPHKQKQSVSANPKORRPSDQGRALPFSNSYSK 425
DB 456 -QDRVSHKKEQSGNLGASALASSTSSASRMITYSSNDQPTQOQSQOQSKTISTSIAXD 514
QY 426 TQSNNAENKRPREDRESGRKASSTAKYPAAPLPGLERK----- 463
DB 515 QCHKRLSRHOTVLMSEKNAHAGATPYTP-DPGEPYAKYGPLOLPLELTHSHLTGYLNG 573
QY 464 -----KTPPTSTNSVLSTSTNR---SNPSPLERASLGQASIQ 499
DB 574 GGEVDASGIPLPWRYTPLPFTAAPAPNSCSTSSRGSRSLSSSSPSRHPVALISLID 633
QY 500 N-----GKDTAPQRPVAPASPSANISSGCGAPRTYPPGVSSRSSTFHA 544
DB 634 NNPBLANLRCREMKEMAGGPGVAGVPLASKQLHQTISEFLIKQSTEDCALLLQOSTAVA 693
QY 545 -GOLRQVRDQONL-----PYGVTPASPS-----GHSQGRGASGIFSXTSKTF 587
DB 694 EGKDDPKKASSVGGVPPASTTPTSTTAPBEGSAPCPBEINGKTKITWSSSSSPFSK- 752
QY 588 VRBNLNE-----PESKDRVETL-----RPHV-----VSGSGDKKEKEFREFA 624
DB 753 --ANLQGSFHYKMSAEASKLFQTLQESPLPVEQRTKRKHVAVGSGNSGSD----- 800
QY 625 KPRSLRFTSMKTTSSMEPEVMREIKVLDANSQSGE 662
DB 801 -----SGOETNDKXNGSDRSSEKVLQAGSSSTD 829
```

RESULT 7

UC7500
qik protein - chicken
N/Alternate names: Qin-induced kinase
C/Species: Gallus gallus (chicken)
C/Date: 17-Nov-2000 #sequence_rev15ion 17-Nov-2000 #text_change 09-Jul-2004
C/Accession: JC7500
R/Xia, Y.; Zhang, Z.; Kruse, U.; Vogt, P.K.; Li, J.
Biochem. Biophys. Res. Commun. 276, 564-570, 2000
A/Title: The new serine-threonine kinase, Qik, is a target of the qin oncogene.
A/Reference number: JC7500
A/Contents: Embryo fibroblasts

A/Accession: JC7500
A/Molecule type: mRNA
A/Residues: 1-798 <XIA>
A/Cross-reference: UNIPROT:Q91A88; GB:AF219232
C/Comment: This protein, a member of the AMPK/SNFI family of serine/threonine kinases,
C/Genetics:
A/Gene: qik
C/Keywords: protein kinase

Query Match 26.3%; Score 981; DB 2; Length 798;
Best Local Similarity 34.4%; Pred. No. 4.5e-30;
Matches 250; Conservative 106; Mismatches 201; Indels 170; Gaps 19;

```
QY 42 TSADEQF-HIGNVRLKTKTGKGFPAVKLARHLTGKEVAVKIIDTQLNSSLQKLFRE 100
DB 14 SAAQPRLRVGFDIRTTGKGFPAVKLARHLTGKEVAVKIIDTQLNSSLQKLFRE 73
QY 101 VRIMKVLNHPNIVKLFVETETKTYLWMEYASGGEVFDYLVAHGMEKEAKAFKQV 160
DB 74 VOIMKVLNHPNIVKLYQWETKMITYEYAFKMGEMFDHLTNGHLSSEAKKFWQIL 133
QY 161 SAVQYCHQKFIYHRDIKAENLLLDADMTKIADFGFSNEFTFQNKLDTFGSPRYAPRL 220
DB 134 SAVEYCHSHIYHRDLKTEVLLDADMTKIADFGGNGFYKSGEPLSTWCGSPRYAPREV 193
QY 221 FQKATDGEVDVWISGLVLLTYVSGSLFPDQNLKELRVRVLRGKRTIPYMWSTDCENL 280
DB 194 FEGKEYEGPHLDIWSGLVLLYVCGSLFPDQNLPLLRQVRLEGRRPIPFMSSEDETL 253
QY 281 LRKFLINPSKGTLEQIMKDRMNYGHEDELEK-----YVEPLPDYKDRPTE 330
DB 254 IRMLVDPPTKRTTIQIKQHKMNA---DPSLRQOQSLSFSQNTNSNLGDTNE-QVLG 309
QY 331 LWSMGYTREIQLDSLVGQRYNEVATYLL-----GYSSSELEGDTT---LKPRPSAD 382
DB 310 IMQTLGIDRQRTVESLQNSYNHFAIYVLLRLKEYSRQSLSPRATGROQRPR-SSS 368
QY 383 LMTSSAP-----SPSHKQKQSVSA-----NPKORRPSDQGRALPFS 419
DB 369 ISNAEMFQDSLSETLRSLLYQFQSLQPSLQAEKDCMNNPLQVPF-----PVDNPF 424
QY 420 N-----SYSKTQSNNAENKRPREDRESGRKA-----SSTAK----- 451
DB 425 NGLPFRKRSISPSLLETTISEEVQKELDEIKAYDHPRIKRSNTSRRTTLAEVTHFY 484
QY 452 -----VPASPLPG-----LEKRTTPTSTNSVLSTSTN 480
DB 485 QHAPCIVISSASPTGEGTSSDCLTSSNDSVALSSCLAGQVMTGSPATAMTSAFLA 544
QY 481 RSNNSLLE-----RASLGQASIQNGK---DSTAPQRPV----- 512
DB 545 SOSDAPVLQVQCMGASLLPVSFQGRASDTSILQGAKAFQOLRKARAKFGLANK 604
QY 513 -----ASPSAHNISSGCGAPDRTPPPGVSSRS---TFH 543
DB 605 IKGFAPQVCOSSSSRAARSAMPFGHAQPPYTCYSSSGSRBERNLLEEVLLQQRMLQLO 664
QY 544 AGQLRQVRDQONLPYGVTPASPSGHSQGRGASGIFSXTSKFVRNINLBPESKORVET 603
DB 665 HHQLLPACPDQTSQTSATNGLPSPSDAGTCXKANSNL---LTSLEQENSEBELAFGNSQL 721
QY 604 LRPHVVG 610
DB 722 LQHPFPG 728
```

RESULT 8

I49072
protein kinase - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_rev15ion 02-Jul-1996 #text_change 16-Aug-2004
C/Accession: I49072
R/Ruitz, J.C.; Conlon, F.L.; Robertson, E.J.

A>Title: A putative protein kinase gene (kin1(+)) is important for growth polarity in *S. cerevisiae*
 A/Reference number: A36474; MUID:91045979; PMID:2236039
 A/Accession: A36474
 A/Status: nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-361; 'R', 363-619; 'I', 621-707; 'W', 709-891 <LE2>
 A/Cross-references: GB:M36060
 C/Genetics:
 A:Gene: kin1+
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology
 C/Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 F:123-395/Domain: protein kinase homology <KIN>
 F:131-139/Region: protein kinase ATP-binding motif

Query Match 21.7%; Score 812.5; DB 2; Length 891;
 Best Local Similarity 28.5%; Pred. No. 1e-23;
 Matches 243; Conservative 117; Mismatches 317; Indels 177; Gaps 24;

```

3  SARTPLFTLNERDTEQ-----PTLGLHDSKPSKSNMIRGNATSADQPH-----IGNY 53
Db  SSKRPDLPASPSRTDHSRLRPVSGH-----SYSADEKREKRVKLVIGNY 125
54  RLKTTIGKGNPAKYKLAARHILTGKEVAKTI-----DKTQLNSSLQKL 97
Db  VLKGTIGAGSWGKYQDAHHLKGTGQPAIKITVRLHPDITKAKAAASAEATKAQSEKNKE 185
98  PRPR---IMKVLNHPINVLFEVIEREKLYLYMEVAGSGEVVDYLVAGRMKEKARA 154
Db  IRTYREALSTLLNHPYICEARDYINSHYVFEFVDGQMDYIISGKKEKQARK 245
155  KFRQVAVQYCHOKFIYHRDLKAENLLLDADNMKIKADFGFNSNFTFGKDLDTFGGSP 214
Db  PERQIGALSYLHONSVAHDLKENTLISKTDGIKIIDGLSNLYRQSLRTFGCSLY 305
215  YAAPELFQKKYDGPEDVWNSGLVILYTVSGSLPFGQNLKELREVRVLRGKYRIFFYMS 274
Db  FAAPBELNAPYIGPEVDWNSFGVILVLCGVKFPDQNSALHAKIKKGYVEPYLS 365
275  TDGNNLKFFLLNPSKRGLEQIMKRMNVNVED-----DELKYYEBLPDYKPPR 328
Db  SDGGLISRLMLVTDPLKRALTEBLNHPMMIRNTEGPPASAPRPSITPL-----DPEI 421
329  TELVWSMGY-----TREIQDSLVGGRYNEVMATYLLLGKSSLEBDITTLKRPRA-D 382
Db  IREMGDFGPPPEYIVELTKVISSEAYQSLAKTGFSGNSADKKSPFEFRIRRAHD 481
383  LTNSSAPSPSHKYORSVSNP-----KORRPSDAG-----PAIPTSNYSKYKT 426
Db  IENPILPSLNMNDIYDAFHLISIVYVSEBRVYEKGMMNRIAKTPVSSVSPVQPT 541
427  QSNNAENKRP-----EDRSGRKASSTAKVPASPLPGLERKKTTPPTSTNSVLST- 478
Db  SYNRUTLPMPBEVVAAYKDESPRVSNTSLARRKPLDTE--SHSPSPSATSSIKKPPSS 539
542  SYNRUTLPMPBEVVAAYKDESPRVSNTSLARRKPLDTE--SHSPSPSATSSIKKPPSS 539
479  -----TNSRNSPLLEBASLQASLQNGKDSAPQORVPVAPASANISSGGAPD 528
Db  IFRPFRSRKONKSSSTLQNSAPL-----ETSGSPPTPRTKPSHKRP---VSYKAKLV 651
600  RTNPPRGVSRSSTFHAQLRQV-----RDOONLPYGV---TPASPSGSGGR 573
529  QSAIGRSTVREGVYAGISSQMDSLNMDSTGPSASMANAPPSVRNNRVNLNPGASLGHG 711
Db  GAGSISKFTSKVVRKNLMEPSKDVETLRPHVVGSGGNDKEKEFRKAPRSLRFTW 633
574  RMTSTSTNR-QKQJLNETGNPVDKN-----STSPSKSTDLDIKVFLKGLF 759
712  SMKTTSMENEMREIRKYLNDANSQ--SELHEKYLMLCM-----GTGHEBPPVQ--- 663
634  SVSTTSTKSTESIQRLMLVGMGLDIYKIKGTY--ACLYKPGQGITTPPKTSVHTTRK 817
760  WEMEVCKLPRLSLNGVAFKISGTSM 710
818  PSYGSNSTDYSVGPVPLDNGSPASNLAEIYIVKVPFLSLGVSFHNRSIGSWQ 877

```

Query 711 EKNIAASKINELKT 724
 Db 878 YKTLASRIINELKT 891

RESULT 11
 A26030
 serine/threonine-specific protein kinase (EC 2.7.1.-) SNF1 - yeast (*Saccharomyces cerevisiae*)
 N/Alternate names: protein YDR477w
 C/Species: *Saccharomyces cerevisiae*
 C/Date: 20-Aug-1987 #sequence_revision 20-Aug-1987 #text_change 09-Jul-2004
 C/Accession: A26030; S69644
 R/Celena, J. L.; Carlson, M.
 Science 233, 1175-1180, 1986
 A>Title: A yeast gene that is essential for release from glucose repression encodes a p
 A/Reference number: A26030; MUID:86289463; PMID:3526554
 A/Accession: A26030
 A/Molecule type: DNA
 A/Residues: 1-633 <CEL>
 A/Cross-references: UNIPROT:P06782; EMBL:M13971; NID:g172629; PIDN:AAA35058.1; PID:g172
 R/Dietrich, F.S.
 Submitted to the EMBL Data Library, August 1995
 A/Description: The sequence of *S. cerevisiae* cosmid 9410, 8035, 8166, and 9787.
 A/Reference number: S69554
 A/Accession: S69544
 A/Molecule type: DNA
 A/Residues: 1-633 <DIE>
 A/Cross-references: EMBL:U03050; NID:g927726; PIDN:AA64904.1; PID:g927733; GSPDB:GN000
 C/Genetics:
 A:Gene: SGD:SNF1; MIPS:YDR477w
 A/Cross-references: SGD:S0002885; MIPS:YDR477w
 A/Map position: 4R
 C/Function:
 A:Description: catalyzes the formation of peptidyl-L-serine-phosphate or peptidyl-L-threonine
 A/Note: required for expression of glucose-repressed genes in response to glucose deple
 C:Superfamily: AMP-activated protein kinase; protein kinase homology
 C/Keywords: ATP; autophosphorylation; magnesium; nucleus; phosphoprotein; phosphotransf
 F:53-306/Domain: protein kinase homology <KIN>
 F:61-69/Region: protein kinase ATP-binding motif
 F:84,103,177,179/Active site: Lys, Glu, Asp, Lys #status predicted
 F:182,186/Binding site: magnesium (Aen, Asp) #status predicted
 F:210/Binding site: phosphate (Thr) (covalent) (by unidentified kinase) #status predict

Query Match 21.3%; Score 797.5; DB 1; Length 633;
 Best Local Similarity 36.0%; Pred. No. 2.6e-23;
 Matches 190; Conservative 94; Mismatches 163; Indels 81; Gaps 12;

```

39  NSATSDQPHIGNYRLKTTIGKGNPAKYKLAARHILTGKEVAKTIIDKQTNSSSLQ-KL 97
Db  NPKSSLADGAHIGNVOIVKTLGSGSGKVLATHTTGGQVAKTIINKVLAASDMQGR 100
41  FREVRIMKVLNHPINVLFEVIEREKLYLYMEVAGSGEVVDYLVAGRMKEKARAKFR 157
98  ERELSTVRLRLRHRIHILKLVDSIKSDEILMVEIYA-GNELFDYIVGRDKMSDEEARFFQ 159
101  QVVSAYQYCHOKFIYHRDLKAENLLLDADNMKIKADFGFNSNFTFGKDLDTFGGSPRYAA 217
158  QVVSAYQYCHOKFIYHRDLKAENLLLDADNMKIKADFGFNSNFTFGKDLDTFGGSPRYAA 217
160  QVVSAYQYCHOKFIYHRDLKAENLLLDADNMKIKADFGFNSNFTFGKDLDTFGGSPRYAA 219
218  PELFOGKKYDGPEDVWNSGLVILYTVSGSLPFGQNLKELREVRVLRGKYRIFFYMSDTC 277
220  PEVTSKLTAGPEVDWNSGVILYVLCRLRPDDSIPLVFNKISNGVTLTKPKFSPGA 279
278  ENLKFFLLNPSKRGLEQIMKRMNVNVEDDELKYYEBLPDYKPPR-----DYKDP 326
280  AGIIRKMLVNLNPSKRGLEQIMKRMNVNVEDDELKYYEBLPDYKPPR-----DYKDP 326
327  RRTPE-----LMVSGYTRERIQDSLVGQR---YNVMAATYLLLGKSSLEBDIT 374
340  DNDEIDNVLNLSSTMGYEKEIYESLESSBDTPAFNEIRDAYML----- 385
375  LKRPESADLTNSAPSPSHKYORSVSNP-----KORRPSDAG-----PAIPTSNYSKYKT 426

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Db      I K E N K S L I K D M K A N K S V S E D L D T F L S G S P ----- P F F Q Q S K S H Q S G Y D H - 431
Qy      435 R P E E R R E G R K A S S - T A K V P A S P L P G L E R K K T T P T S T N S V L S T S T R S N S S P L E R A S 492
           :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      432 - - E T A K O H A R R M A S A I T O Q R T Y H O S P F M D O Y K - E E D S T V S I L T S L ----- P Q I H R A N 481
           :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Qy      493 L Q A S I O N G K D S T A P Q V R V P A S P S A H N I S S G G A P D R T N P F R G V S R S 540
           :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      482 M ----- L A Q S P A A S K I S P L V T K S K R M H F G I R S R S 513

RESULT 12
T20941
hypothetical protein F15A2.6 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C.Accession: T20941
R.Gregory, J.
submitted to the EMBL Data Library, March 1996
A.Reference number: Z19349
A.Accession: T20941
A.Status: preliminary; translated from GB/EMBL/DBD
A.Molecule type: DNA
A.Residues: 1-887 <Wtl>
A.Cross-references: UNIPROT:Q19469, EMBL:Z70207, PIDD:CAA94127.1, GSPDB:GND00028, CESP:PL
A.Experimental source: clone F15A2
C.Genetics:
A.Gene: CESP:F15A2.6
A.Map position: X
A.Introns: 32/1; 63/3; 92/2; 139/2; 189/3; 328/2; 448/2; 516/3; 604/2; 684/3; 735/2; 777/

```

```

Query March 20.8%; Score 778.5; DB 2; Length 887;
Best Local Similarity 29.5%; Pred. No. 1.9e-22;
Matches 221; Conservative 139; Mismatches 273; Indels 115; Gaps 23;

QY 49 HIGNYRLTKTGKGNFAKVKLARHILTGKEVAVKIIDTKLTNSSLOKLFREYRIMVLN 108
Db 16 YCGPYKLEKTLGKQGTGLVKTGTHCITGRKVALITVAKETLSBVLÖKVERELAIKLTIE 75
QY 109 HPNIVKLFVETETKTYLVMEVYASGGEVPDYLVAHGRMKEKEARAKFQVVASVOYCHQ 168
Db 76 HPHVHLHYDVYENKRYLYLLEHVSGGELPDYLRKRRLMSKEARKPFROIIISALFCHIA 135
QY 169 KFIYHDLTKAENLLDADNMNIIKIDPFNSFEFTGNLIDFEGSSPPVAAEELÖGKKYKG 228
Db 136 HNIHRDLKPENLILDERNNIKVADFGMASIQVBSMLETSCSPHYACCEVATVIRGEYTD 195
QY 229 PEVDVMSLGVIYLYTVSGLPEFDQNLKEILREYLRGKRIIPYMSDCENLILKELILIN 288
Db 196 RKADVMSCGVILYALTVGALPFDDDNLRNLEKVRGCVFHI PHFVPADVGSLLRAMI EVD 255
QY 289 PSKRGTLEQIMKDRMNA-VGHEDEL-----KPYEVLPRYKPPRELTAVSNG--Y 337
Db 256 FGKRYSLADYFKHFWASGTTKPADELELPMNSQVYQTHVIGDESIDPDLRHNNCIGCRK 315
QY 338 TREEDISLVGQRYN-EVMATYLLIGYSSB--LEGDT-ITLK-----PRPSADLTN 385
Db 316 DKQULINELLSPKHNTEKMYVFLILDRKRRRPAQEDDTEVLVGAQONNDPPKRRDSSR 375
QY 386 SS-----APSPSHVÖRSVSNAPKORFSDQAPAIPTSNYSKK--TÖSNMAENKR 435
Db 376 TSRYPMGISIDGSPINPRKTYGRNÖKSGRRSSLGSPTESPRSTBDLFSSSSGSYSAR 435
QY 436 PEEDREGGRASSTAK-----VPASPLPDLF-----RKTTYPTSTNSVLTSTYRSKN 484
Db 436 AGEERDGRGRASSTNSYHYTTPVDPÖTLAEARHVRDAQÖERERSDRGSGRSKESXD 495
QY 485 SPLLERASLOASIONGKOSTA--PÖRVVYAPSAHNISSGGAAPRTNPFPRVGRSRSTF 542
Db 496 R---SDKSSASSCKNDASSTSSVPHKYPRPSVMSSESVVVSSSTNMSTN-----SSTNL 547
QY 543 HAQQLAQVDDQNLPGVTPASPSGHSÖGRKASGSI FSKE--TSKFVRRLNPEPSKOR 600

```

[illegible][illegible]

Db 479 KKRQLKSLVLP-GEPANVLS-----PER-----RCKSVELDNQAH-- 514
Qy 561 TPASPSGSHSGRRGASISIFSKFTSKVVRNLNAPESKDRVETLRPHVVGSGGNDKEKE 620
Db 515 -----IDSAQKKKGA--KVFGS-----LERGLDK-----MITMLTP-----SKRGKY 549
Qy 621 PREAKPSRLPRTWMTKTTSSMEPMEMRETRKVLNANSCSELHEKMLCMHTPGHD 680
Db 550 TREB-PKRLRAHVHVTNTINVPQALNQLVRLVPSKNV-DYVKGITLTKCKTQSDPKV 607
Qy 681 FVQWEMEVCKLPRLSLNGVRFKRISGTSMAPKNIASKIANELK 724
Db 608 TMQPELEVCSLSEVVGIRQRRLKGDAMVYKRLVEIDLSCKV 651

RESULT 14

872513
C;Species: Kluyveromyces marxianus var. lactis, Candida bphaerica
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C;Accession: S72513
R;Ggffintl, P.; Ficaeall, A.; Domini, C.; Lodi, T.; Puglisi, P.P.; Ferrero, I.
Curr. Genet. 29, 316-326, 1996
A;Title: FOG1 and FOG2 genes, required for the transcriptional activation of glucose-reg
A;Reference number: S72513, MUID:96171514, PMID:8538052
A;Accession: S72513
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-6d2 <GOF>
A;Cross-references: UNIPROT:P87209
A;Note: the source is designated as Kluyveromyces lactis
C;Geneticb
A;Gene: FOG2
C;Function:
A;Description: probably involved in the regulation of glucose-repressible gene expressio
C;Superfamily: AMP-activated protein kinase; protein kinase homology
P;33-286/Domain: protein kinase homology <Kin>

Query Match 20.7%; Score 775; DB 2; Length 602;

Best Local Similarity 37.3%; Pred. No. 1,7e-22;
Matches 187; Conservative 83; Mismatches 157; Indels 74; Gaps 12;

Qy 27 KPSKSMNIRGRNATSDAEPHTGNRLKTIKGNPAKYKLABHILTGKAVKTIKD 86
Db 9 QPHGSGQHNRQRLTHRAQGHQIKYQIKTLGSGFSGKVLAYHISTQKVALKINK 68
Qy 87 TOLNSSLQ-KLFEVRIMKVLNPNIVKLFEVETETKTLVLMVYASGGEVFDYLAHG 145
Db 69 KVLAKSMQGRIEREISYLRHLRPHILKLYDKSDEITIMVETV-GNELFDYIVQRD 127
Qy 146 RMKEKRAKFRQVSAVOYCHQKFIYHRDLKAEMLLDADNMKIDAFGSNEFTGK 205
Db 128 KMPQEARFRFOQIISAVDYCHRHKIVHRDLKPEMLLDLHNLVAKIDFGLSNIMTDGNF 187
Qy 206 LDFTCGSPPTAARPLFGQKTYDGPVWVSLGVILYTVSGSLPFDQONLKELEKRLRG 265
Db 188 LKTSQSGPNYAARPVISGKYAGPEVWVSGVILYMLCRRLPFDDESIPLFKINSNG 247
Qy 266 KYRIPFVWSTDCBULLKKFLILNPSKRGTLQIMKDMVMVGHEDDLKPYVEPLPYKD 325
Db 248 VYTFPNLISQGAASLIKMLIVNPNRITVHEIMQDMFVY-----DLFDYLV 295
Qy 326 P-----RTE-----LMVSMGYTREEDISLVGQR-----YNE 353
Db 296 PAESTHQENSESKTEDGSPVLELIDSLVQTLSTMTGVDVDEIVALESDDEDHPSLNE 355
Qy 354 VMATYLLLGYSKSLBEDDTTLKRPASADLTNSAPSPSHKVGQSVANP--KORRSDQ 411
Db 356 IRDAYQILI--KENNLINDIKVNRQGSNDLDTLSQSP--TFEQSLHAPGSKNRH---- 408
Qy 412 AGPAIPTSNYSKKTQGSNNNAENKRPEDRSGRKAASSTAKVPASPLPGLERKKTTPPST 471

Db 409 -----SHRSKRTQORTQYHYNGSGD-----GDSTIALPSSLPQIHR-----A 449
Qy 472 NSYLSSTYTRNSRNSPLERAS 492
Db 450 NMVAGSGQAAMAKISPLSVKKS 470

RESULT 15

T52633
N;Alternate names: SNF1 protein kinase omolog AKIN11
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
C;Accession: T52633
R;Bhalerao, R.P.; Salchert, K.; Bako, L.; Okresz, L.; Szabados, L.; Muranaka, T.; Machi
Proc. Natl. Acad. Sci. U.S.A. 96, 5322-7, 1999
A;Title: Regulatory interaction of PRL1 WD protein with Arabidopsis SNF1-like protein k
A;Reference number: Z25116, MUID:99238528, PMID:10220464
A;Accession: T52633
A;Status: preliminary; translated from GB/EMBL/DBD
A;Molecule type: mRNA
A;Residues: 1-512 <BHA>
A;Cross-references: UNIPROT:P92958; EMBL:X99279; PIDN:CAA67671.1
A;Experimental source: cultivar Columbia
C;Genetics:
A;Gene: AKIN11
C;Function:
A;Description: EC 2.7.1.-; serine/threonine-specific protein kinase AKIN11 [validated,
complements SNF1 mutations in yeast
C;Superfamily: AMP-activated protein kinase; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

Query Match 20.3%; Score 757.5; DB 2; Length 512;

Best Local Similarity 42.9%; Pred. No. 6.6e-22;
Matches 152; Conservative 74; Mismatches 99; Indels 29; Gaps 7;

Qy 37 GRNSATSADQPHIGVRLKTIKGNPAKYKLABHILTGKAVKTIKDTONSSSL-Q 95
Db 9 GNNGVESI-----LPNKLGLKTLGIGSPGKVKLAENHVVTGKVALIKLNRRKIKNMEMEE 63
Qy 96 KLFEVRIMKVLNPNIVKLFEVETETKTLVLMVYASGGEVFDYLAHGMRKEKARAK 155
Db 64 KYRREIKILRLFMHNPRIHQVEYIETSDIYVMEVYKSGELFDYIVKGRQLDEDEARNF 123
Qy 156 FROVSAVOYCHQKFIYHRDLKAEMLLDADNMKIDAFGSNEFTGKLDFTCGSPPY 215
Db 124 FQIISGVEXCHNMVVRHDLKPEMLLDLDRCNKIADFLGSVMRDGHFLKTSQSPNY 183
Qy 216 AAEPLQGGKKYDGPVWVSLGVILYTVSGSLPFDQONLKELEKRLRGKYLIPYMS 275
Db 184 AAEVVISGKLYAGPEVWVSGVILYALLCGTLPPDENIPNLFKIKGDIYTLPSHLSS 243
Qy 276 DCENLLKKFLILNPSKRGTLQIMKDMVMVGHEDDLKPY--VEPLPYKDPDR----- 328
Db 244 EARDLIPMLIVDPVGRITIPRIQRHWPQT-----HLRPIYLVSP--PDVDEAKKINE 297
Qy 329 -TELMVSMGYTREEDISLVGQRYNEVMATYLL-----GYKSSLEIGDT 372
Db 298 IYQEVVNMGFDRIQVLESJLNRQNDATVYVYLLDNRFRVPFGYLESFQET 351

Search completed: February 26, 2005, 17:52:13
Job time : 50 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2005, 17:34:27 / Search time 177 Seconds

(without alignments)
2094,606 Million cell updates/sec

Title: US-10-760-407-2

Perfect score: 3737

Sequence: 1 MSGARTPLPLNREDEQPT.....SGTSMAPKNIASKIANELK 724

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3654	97.8	722	2	008679 ratius norv
2	3654	97.8	722	2	06PDR4 mus musculu
3	3647.5	97.6	719	2	068A18 homo sapien
4	3624	97.0	778	2	096HB3 mus musculu
5	3598	96.3	888	2	08BR95 mus musculu
6	3566	95.4	691	2	096R00 mus musculu
7	3515	94.1	745	2	015524 mus musculu
8	3504	93.8	755	2	07KZ17 homo sapien
9	3467	92.8	774	1	MRK2 MOUSE
10	3195.5	85.5	776	2	07ZYL7 xenopus lae
11	3188	85.3	785	2	08QGV3 xenopus lae
12	3027	81.0	780	2	08Q4P1 xenopus lae
13	2561	68.5	795	2	08VH5 mus musculu
14	2555	68.4	793	2	08B678 mus musculu
15	2546	68.1	795	2	09P012 mus musculu
16	2523.5	67.5	792	2	06INT7 xenopus lae
17	2493	66.7	771	2	069Z17 mus musculu
18	2398.5	64.2	744	1	MRK3 HUMAN
19	2395.5	64.1	776	2	09P251 mus musculu
20	2379	63.7	729	2	09JKE4 mus musculu
21	2374	63.6	725	2	08Q4T2 xenopus lae
22	2374	63.5	727	2	08VH0 ratius norv
23	2078	55.6	792	2	08Q2W0 brachydanio
24	1950	52.2	659	2	086T8 homo sapien
25	1940.5	51.9	752	1	MRK4 HUMAN
26	1938.5	51.9	752	1	08C1F4 mus musculu
27	1932.5	51.7	752	2	08NG37 xenopus lae
28	1902	50.9	594	2	06PA64 xenopus lae
29	1902	50.9	704	2	07PKD5 anopheles g
30	1894	50.7	938	2	Q9V8V8 drosoephila

32	1878.5	50.3	638	2	Q96SM9	Q96SM9 homo sapien
33	1830.5	49.0	905	2	Q7KRK5	Q7KRK5 drosoephila
34	1826	48.9	1138	2	Q7KRK3	Q7KRK3 drosoephila
35	1820.5	48.7	1075	2	Q95U75	Q95U75 drosoephila
36	1818	48.6	1066	2	Q8MVX0	Q8MVX0 haemochus
37	1782.5	47.7	1096	2	Q17368	Q17368 caenorhabd
38	1771.5	47.4	1192	2	Q9TW45	Q9TW45 caenorhabd
39	1765.5	47.2	1192	2	Q17346	Q17346 caenorhabd
40	1710.5	45.8	966	2	Q8MVX2	Q8MVX2 haemochus
41	1587	42.5	634	2	Q80T81	Q80T81 mus musculu
42	1556.5	41.7	1046	2	Q7YU80	Q7YU80 drosoephila
43	1552	41.5	993	2	Q7KRK4	Q7KRK4 drosoephila
44	1551	41.5	833	2	Q6NPA6	Q6NPA6 drosoephila
45	1550.5	41.5	1058	2	Q96J35	Q96J35 drosoephila

ALIGNMENTS

RESULT 1

008679 ID 008679 PRELIMINARY; PRT; 722 AA.
AC 008679;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Serine/threonine kinase.
GN Name=mark2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=97262070; PubMed=9108484; DOI=10.1016/S0092-8674(00)80208-1;
RA Drewes G., Ebnech A., Preuss U., Mandelkow E.;
RT "MARK - a Novel Family of Protein Kinases that Phosphorylate
RT Microtubule-associated Proteins and Trigger Microtubule Disruption";
RL Cell 89:297-308 (1997).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RA Drewes G., Ebnech A., Preuss U., Mandelkow E.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; Z83869; CAB06295.1; -.
DR HSSP; P24941; IOIO.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_Cterm.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR InterPro; IPR000449; UBA.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00627; UBA; 1.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00165; UBA; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_STR; 1.
DR PROSITE; PS00030; UBA; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 722 AA; 80871 MW; 2CBAPD1C38007ECC CRC64;

Query Match 97.8%; Score 3654; DB 2; Length 722;
Best Local Similarity 97.8%; Pred. No. 1.8e-170;

Matches	708;	Conservative	9;	Mismatches	5;	Indels	2;	Gaps	1;
Qy	1	MSARTPLPTINERTTEOPTLGHIDSKRSPSSNMIRGNSATSDADPHIGNYRLTKTIG	60						
Db	1	MSARTPLPTINERTTEOPTLGHIDSKRSPSSNMIRGNSATSDADPHIGNYRLTKTIG	60						
Qy	61	KGNFAKVKLARHILTGKEVAVKIIDKTQLNSSSLOKLFREVRIMKVLNHPNIVLFEVIE	120						
Db	61	KGNFAKVKLARHILTGKEVAVKIIDKTQLNSSSLOKLFREVRIMKVLNHPNIVLFEVIE	120						
Qy	121	TEKTLYLWMEYASGGEVFDYLVAGRMKEKARAFKQVSAVOYCHQKFTVHBDLKAEN	180						
Db	121	TEKTLYLWMEYASGGEVFDYLVAGRMKEKARAFKQVSAVOYCHQKFTVHBDLKAEN	180						
Qy	181	LILADANNIKIADGFSENEFTFGNKLDTFGCSPPYAAPELFQGGKYGPEVDWVSLGVTL	240						
Db	181	LILADANNIKIADGFSENEFTFGNKLDTFGCSPPYAAPELFQGGKYGPEVDWVSLGVTL	240						
Qy	241	YTLVSGSLPFDGQNLKEIRERVLNKGKRIPIPYMSTDCENLLKKEFLINPSKRGTLBQIMK	300						
Db	241	YTLVSGSLPFDGQNLKEIRERVLNKGKRIPIPYMSTDCENLLKKEFLINPSKRGTLBQIMK	300						
Qy	301	DRMNVGHEDDELKPYVEPLPDYODPRTELAMSMGYTREBIODSLVGQRYNEVMATYLL	360						
Db	301	DRMNVGHEDDELKPYVEPLPDYODPRTELAMSMGYTREBIODSLVGQRYNEVMATYLL	360						
Qy	361	LGYSSELEGGDTILKRPSPADLTNSAPSPSHKVSANPKORFSDOAPALPTSN	420						
Db	361	LGYSSELEGGDTILKRPSPADLTNSAPSPSHKVSANPKORFSDOAPALPTSN	420						
Qy	421	SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTTPPTSTNSLSTSN	480						
Db	421	SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTTPPTSTNSLSTSN	480						
Qy	481	RSNSPLLEASLGQASIQNGKSTAQRPVAPVSPSAHNTSSSGAGADRTNPRGVSRS	540						
Db	479	RSNSPLLEASLGQASIQNGKSTAQRPVAPVSPSAHNTSSSGAGADRTNPRGVSRS	538						
Qy	541	TFHAGQLRQVRDQNLPGYVTPAPSPSGHSGRGASGISTSKTSPKVRNLTNLEPSKOR	600						
Db	539	TFHAGQLRQVRDQNLPGYVTPAPSPSGHSGRGASGISTSKTSPKVRNLTNLEPSKOR	598						
Qy	601	VELTRPHVVGSGGNDKEKEFEAKPRSLRFTWSMKTSSMBENEMWREIRKVLANDNSQ	660						
Db	599	VELTRPHVVGSGGNDKEKEFEAKPRSLRFTWSMKTSSMBENEMWREIRKVLANDNSQ	658						
Qy	661	SELHEKMTLCMGTPHEHPVQWEMEVCLPRLSLNGVAFKISGTSNAFKIASKIAN	720						
Db	659	SELHEKMTLCMGTPHEHPVQWEMEVCLPRLSLNGVAFKISGTSNAFKIASKIAN	718						
Qy	721	ELKLI 724							
Db	719	ELKLI 722							

RESULT 2

ID	Q6PDR4	PRELIMINARY;	PRT;	722 AA.
AC	06PDR4;			
DT	05-JUL-2004 (T-REMBLrel. 27, Created)			
DT	05-JUL-2004 (T-REMBLrel. 27, Last sequence update)			
DE	Mark2 protein.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feigold E.A., Grouse L.H., Derge J.G.,			
RA	Klauniger R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,			

RA	Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatlenko U., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA	Scapletemo M., Soares M.B., Ronaldo M.F., Casavant T.L., Schaefer T.E.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loguelli N.A., Peters G.J., Abramson R.D., Mallya S.J.,
RA	Bosch S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Vyllion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimm J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA	Jones S.J., Marra M.A.,
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences."
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
RA	Strausberg R.,
RA	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC	-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR	EMBL; BC058556; AAH58556.1; -.
DR	HSSP; 063450; 1A06.
DR	GO; GO:0005524; F:ATP binding; IEA.
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR	GO; GO:0016740; F:transferase activity; IEA.
DR	GO; GO:000468; P:protein amino acid phosphorylation; IEA.
DR	InterPro; IPR001772; kinase Cterm.
DR	InterPro; IPR01009; kinase_like.
DR	InterPro; IPR000719; prot_kinase.
DR	InterPro; IPR002290; Ser_thr_kinase.
DR	InterPro; IPR008271; Ser_thr_kinase.
DR	InterPro; IPR001245; Tyr_kinase.
DR	InterPro; IPR000449; UBA.
DR	Pfam; PF02149; K41; 1.
DR	Pfam; PF00069; pkinase; 1.
DR	Pfam; PF00627; UBA; 1.
DR	ProDom; PD000001; Prot_kinase; 1.
DR	SMART; SM00220; S_TKc; 1.
DR	SMART; SM00219; TyrKc; 1.
DR	SMART; SM00165; UBA; 1.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR	PROSITE; PS00030; UBA; 1.
KW	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ	SEQUENCE 722 AA; 80873 MW; 10694F53CB96EA27 CRC64;
Qy	Query Match
Qy	Best Local Similarity 97.8%; Score 3654; DB 2; Length 722;
Qy	Matches 708; Conservative 9; Mismatches 5; Indels 2; Gaps 1;
Qy	1 MSARTPLPTINERTTEOPTLGHIDSKRSPSSNMIRGNSATSDADPHIGNYRLTKTIG
Db	1 MSARTPLPTINERTTEOPTLGHIDSKRSPSSNMIRGNSATSDADPHIGNYRLTKTIG
Qy	61 KGNFAKVKLARHILTGKEVAVKIIDKTQLNSSSLOKLFREVRIMKVLNHPNIVLFEVIE
Db	61 KGNFAKVKLARHILTGKEVAVKIIDKTQLNSSSLOKLFREVRIMKVLNHPNIVLFEVIE
Qy	121 TEKTLYLWMEYASGGEVFDYLVAGRMKEKARAFKQVSAVOYCHQKFTVHBDLKAEN
Db	121 TEKTLYLWMEYASGGEVFDYLVAGRMKEKARAFKQVSAVOYCHQKFTVHBDLKAEN
Qy	181 LILADANNIKIADGFSENEFTFGNKLDTFGCSPPYAAPELFQGGKYGPEVDWVSLGVTL
Db	181 LILADANNIKIADGFSENEFTFGNKLDTFGCSPPYAAPELFQGGKYGPEVDWVSLGVTL
Qy	241 YTLVSGSLPFDGQNLKEIRERVLNKGKRIPIPYMSTDCENLLKKEFLINPSKRGTLBQIMK
Db	241 YTLVSGSLPFDGQNLKEIRERVLNKGKRIPIPYMSTDCENLLKKEFLINPSKRGTLBQIMK

|||||
Db 241 YTLVSGSLPFDGQNLKELRERVLGRKRIIPFYWSTDCENLKKFLINPSKRGTLBQIMK 300
Qy 301 DRMMNVGHEDDELKPYVEPLPDYKDPRTTELWVSMGYTREIEIDSLVGQRVNEVMATYLL 360
Db 301 DRMMNVGHEDDELKPYVEPLPDYKDPRTTELWVSMGYTREIEIDSLVGQRVNEVMATYLL 360
Qy 361 LGYKSSLEGGDTTLTKRPSADLTNSAPSPSHKVQSVANPKQRFSPQAGPATYTSN 420
Db 361 LGYKSSLEGGDTTLTKRPSADLTNSAPSPSHKVQSVANPKQRFSPQAGPATYTSN 420
Qy 421 SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLTSTN 480
Db 421 SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLTSTN 480
Qy 481 RSRNSPLLERASLGGASLQNGKOSTAPQVVPASPSAHNISSSGAGBDRTNPRGVSSRS 540
Db 479 RSRNSPLLERASLGGASLQNGKOSTAPQVVPASPSAHNISSSGAGBDRTNPRGVSSRS 538
Qy 541 TFHAGQLRQVRDQONLPYGVTPASPSGHSQGRGASGISFSKTSKVFVRNINPEBSKDR 600
Db 539 TFHAGQLRQVRDQONLPYGVTPASPSGHSQGRGASGISFSKTSKVFVRNINPEBSKDR 598
Qy 601 VETLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTSSMBPNEMMRERIRKVLDAVNSCQ 660
Db 599 VETLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTSSMBPNEMMRERIRKVLDAVNSCQ 658
Qy 661 SBLHEKXYMLCMHGTPGHEDFVQWEMEVCKLPRLSLNGVRFKRIISGTSMAFKQIASKIAN 720
Db 659 SBLHEKXYMLCMHGTPGHEDFVQWEMEVCKLPRLSLNGVRFKRIISGTSMAFKQIASKIAN 718
Qy 721 ELKL 724
Db 719 ELKL 722

RESULT 3

068A18 PRELIMINARY; PRT; 719 AA.
ID 068A18;
AC 068A18;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Serine/threonine kinase.
DN Name=Mark2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISUB=Kldney;
RA Sugiyama A., Inoue H., Oka M.;
RT "Homo sapiens mRNA";
RL Submitted (JUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB188493; BAD3741.1; -
DR GO; GO:0016301; F:Kinase activity; IEA.
DR InterPro; IPR001772; Kinase_Cterm.
DR InterPro; IPR011009; Kinase_Like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Chr_kinase.
DR InterPro; IPR008271; Ser_Chr_kin_AS.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR000449; UBA.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; Kinase; 1.
DR Pfam; PF00627; UBA; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYKIC; 1.
DR SMART; SM00165; UBA; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.

DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50030; UBA; 1.
KW Kinase.
SQ SEQUENCE 719 AA; 80646 MW; EC39154CF73E958 CRC64;
Query Match 97.6%; Score 3647.5; DB 2; Length 719;
Best Local Similarity 98.1%; Pred. No. 3.7e-170;
Matches 711; Conservative 4; Mismatches 3; Indels 7; Gaps 2;

Qy 1 MSSARPLPTLNEDTEOPTLGHLDSPSSKSNMIRGNSATSADDEQPHIGNYRLKTTIG 60
Db 1 MSSARPLPTLNEDTEOPTLGHLDSPSSKSNMIRGNSATSADDEQPHIGNYRLKTTIG 60
Qy 61 KGNFAVKLARHILTGKEVAVKIIDTQUNSSSLQCLFREVRIMKVLNHPNIVKLFVIE 120
Db 61 KGNFAVKLARHILTGKEVAVKIIDTQUNSSSLQCLFREVRIMKVLNHPNIVKLFVIE 120
Qy 121 TEKTLVLYMEYASGGVFDVLVAHGMKEEAKRQVAVAVOYCHQKFTVHRDLKAEN 180
Db 121 TEKTLVLYMEYASGGVFDVLVAHGMKEEAKRQVAVAVOYCHQKFTVHRDLKAEN 180
Qy 181 LLLDADNMIKIADFGFNEFTFGNKLDTFCGSPPYAAPLFGQKTDGPEVDVMSLGVL 240
Db 181 LLLDADNMIKIADFGFNEFTFGNKLDTFCGSPPYAAPLFGQKTDGPEVDVMSLGVL 240
Qy 241 YTLVSGSLPFDGQNLKELRERVLGRKRIIPFYWSTDCENLKKFLINPSKRGTLBQIMK 300
Db 241 YTLVSGSLPFDGQNLKELRERVLGRKRIIPFYWSTDCENLKKFLINPSKRGTLBQIMK 300
Qy 301 DRMMNVGHEDDELKPYVEPLPDYKDPRTTELWVSMGYTREIEIDSLVGQRVNEVMATYLL 360
Db 301 DRMMNVGHEDDELKPYVEPLPDYKDPRTTELWVSMGYTREIEIDSLVGQRVNEVMATYLL 360
Qy 361 LGYKSSLEGGDTTLTKRPSADLTNSAPSPSHKVQSVANPKQRFSPQAGPATYTSN 420
Db 361 LGYKSSLEGGDTTLTKRPSADLTNSAPSPSHKVQSVANPKQRFSPQAGPATYTSN 420
Qy 420 NSYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLTST 479
Db 421 NSYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLTST 480
Qy 480 NRSRNSPLLERASLGGASLQNGKOSTAPQVVPASPSAHNISSSGAGBDRTNPRGVSSR 539
Db 481 NRSRNSPLLERASLGGASLQNGKOSTAPQVVPASPSAHNISSSGAGBDRTNPRGVSSR 540
Qy 540 STFHAGQLRQVRDQONLPYGVTPASPSGHSQGRGASGISFSKTSKVFVRNINPEBSK 599
Db 541 STFHAGQLRQVRDQONLPYGVTPASPSGHSQGRGASGISFSKTSKVFVRNINPEBSK 599
Qy 600 RVETLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTSSMBPNEMMRERIRKVLDAVNSC 659
Db 600 -----RPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTSSMBPNEMMRERIRKVLDAVNSC 654
Qy 660 QSEIHKXYMLCMHGTPGHEDFVQWEMEVCKLPRLSLNGVRFKRIISGTSMAFKQIASKIA 719
Db 655 QSEIHKXYMLCMHGTPGHEDFVQWEMEVCKLPRLSLNGVRFKRIISGTSMAFKQIASKIA 714
Qy 720 NELKL 724
Db 715 NELKL 719

RESULT 4

096HB3 PRELIMINARY; PRT; 778 AA.
ID 096HB3;
AC 096HB3;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE MARK2 protein (Fragment).
GN Name=Mark2;
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Krausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueidi T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzyzanski M.I., Skalka U., Smalins D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Strausberg R.,
 RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; BC008771; AA08771.2; -.
 DR PIR; G01025; G01025.
 DR HSP; P24941; IOIO.
 DR Inact; Q96HB3; -.
 DR Genew; HENC3332; MARK2.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:Protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:Protein-tyrosine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR001772; Kinase_Cterm.
 DR InterPro; IPR011009; Kinase_Like.
 DR InterPro; IPR00719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR008271; Ser_thr_kin_AS.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR000449; UBA.
 DR Pfam; PF02149; KAI; 1.
 DR Pfam; PF00069; Kinase; 1.
 DR Pfam; PF00627; UBA; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; S_TKc; 1.
 DR SMART; SM00165; UBA; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00300; UBA; 1.
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 KW NON_TER
 FT
 SQ SEQUENCE 778 AA; 86868 MW; 557691C4CDB617A CRC64;

Query Match 97.0%; Score 3624; DB 2; Length 778;
 Best Local Similarity 91.6%; Pred. No. 5,7e-169;
 Matches 713; Conservative 1; Mismatches 0; Indels 64; Gaps 3;

QY 11 LNERDTEOPTGLHDSKSSKSNIRGNATSADDEPHIGNVLLTIGKGNFAKYKLA 70
 DB 1 LNERDTEOPTGLHDSKSSKSNIRGNATSADDEPHIGNVLLTIGKGNFAKYKLA 60

QY 71 RHILTGKAVAKIITDKQTNSSLOKLFREYRIMKVLNHPNIVKLFEYIETEKTLVYME 130
 DB 61 RHILTGKAVAKIITDKQTNSSLOKLFREYRIMKVLNHPNIVKLFEYIETEKTLVYME 120
 QY 131 YASGEVEFDYVAHGRMEKEKARAFQVSAVOYCHOKFTVHRDLKAENLLDADNMIK 190
 DB 121 YASGEVEFDYVAHGRMEKEKARAFQVSAVOYCHOKFTVHRDLKAENLLDADNMIK 180
 QY 191 IADPGFSNEFTFGNKLDFPCGSPPIAABELQGGKYDDPEVDWMSGLVTLVSGSLPF 250
 DB 181 IADPGFSNEFTFGNKLDFPCGSPPIAABELQGGKYDDPEVDWMSGLVTLVSGSLPF 240
 QY 251 DQONLKELRERVLRGKVIIPFYMSDTCENLLKKFLLNPSKRGTLQIMKRMNVGHED 310
 DB 241 DQONLKELRERVLRGKVIIPFYMSDTCENLLKKFLLNPSKRGTLQIMKRMNVGHED 300
 QY 311 DELAKYVEPLPYDKPRRTLMVMSGYTRREIQDSLVGQRVNEVATYLLIGYKSSLEIG 370
 DB 301 DELAKYVEPLPYDKPRRTLMVMSGYTRREIQDSLVGQRVNEVATYLLIGYKSSLEIG 360
 QY 371 DTTTLKPRPSADLTNSAPSPSHKQVSANPKQRRRSDQ-AGPAIPTNSYSKKTQSN 429
 DB 361 DTTTLKPRPSADLTNSAPSPSHKQVSANPKQRRRSDQ-AGPAIPTNSYSKKTQSN 420
 QY 430 NAENKRPEDRESGRKASSTAKVPASPLGLERKKTTPPTSTNSVLTSTNRSRNSPLLE 489
 DB 421 NAENKRPEDRESGRKASSTAKVPASPLGLERKKTTPPTSTNSVLTSTNRSRNSPLLE 480
 QY 490 RASLGQASIQNGKD----- 503
 DB 481 RASLGQASIQNGKDSLTPGSPASTASAAVASAPRQHKQKMSGVHPNKAAGLPTE 540
 QY 504 -----STAPQRPVAPSPSAHNTSSSGGAPDRTPNPGVSSRSTPHAGOLROYRDOON 555
 DB 541 SNCEVPRPSTAPQRPVAPSPSAHNTSSSGGAPDRTPNPGVSSRSTPHAGOLROYRDOON 600
 QY 556 LPYGVTPASPSPGSHSGRRGASGISFSKFTSKFV-----RRNINEBSKDRVETLRP 606
 DB 601 LPYGVTPASPSPGSHSGRRGASGISFSKFTSKFVRRNINEBSKDRVETLRP 660
 QY 607 HVGSGGNDKEXEERREKAPRSLRTWMSKTTSSMEPNMREIRKVDANCCOSELHEK 666
 DB 661 HVGSGGNDKEXEERREKAPRSLRTWMSKTTSSMEPNMREIRKVDANCCOSELHEK 720
 QY 667 YMLLCMHGTPGHEDPFQWEMEVCXLPRLSLNGVRFKRLISGTMAFNKISKIANELKL 724
 DB 721 YMLLCMHGTPGHEDPFQWEMEVCXLPRLSLNGVRFKRLISGTMAFNKISKIANELKL 778

RESULT 5
 OGBR95 PRELIMINARY; PRT; 888 AA.
 AC OGBR95;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2004 (TrEMBLrel. 23, last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 23, last annotation update)
 DE Mus musculus 9-5 days embryo parthenogenote cDNA, RIKEN full-length
 DE enriched library, clone:B13006516 product:ELKL motif kinase, full
 DE insert sequence. (Fragment).
 GN Name=Mark2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium; PubMed=11217851; DOI=10.1038/35055500;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RA The RIKEN Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 Kono H., Ozaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtractions of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 Kono H., Akiyama J., Nishi K., Kitagawa T., Tashiro H., Itoh M.,
 Sumi T., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 Fujisawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsumoto M.,
 Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 Ozaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RA Adachi J., Aizawa K., Akimura T., Aikawa T., Bono H., Carninci P.,
 Fukuda S., Furumoto M., Hanagaki T., Hara A., Hashizume W.,
 Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 Horii Y., Imclanti K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 Nishi K., Nomura K., Numazaki R., Ono M., Ohata N., Ozaki Y.,
 Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC - SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL: AK045329; BAC32312.1; -.
 DR HSP: P24941; 1010.
 DR MGD: MGI:96538; Mark2.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:Protein serine/threonine kinase activity; IEA.
 DR GO: GO:0016740; F:Transferase activity; IEA.
 DR GO: GO:0006468; P:Protein amino acid phosphorylation; IEA.
 DR InterPro: IPR011772; Kinase_Cterm.
 DR InterPro: IPR011009; Kinase_Like.
 DR InterPro: IPR000719; Prot_Kinase.
 DR InterPro: IPR002290; Ser_Thr_Kinase.
 DR InterPro: IPR008271; Ser_Thr_Kinase.
 DR InterPro: IPR000449; UBA.
 DR Pfam: PF02149; KAI; 1.
 DR Pfam: PF00069; Kinase; 1.
 DR Pfam: PF00637; UBA; 1.
 DR ProDom: PD000001; Prot_Kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00165; UBA; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE: PS00108; PROTEIN_KINASE_SF; 1.
 DR PROSITE: PS50030; UBA; 1.
 KR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 FT NON_TER 888 888
 SQ SEQUENCE 888 AA; 98822 MW; 07C8F23520F80CD CRC64;
 Query Match 96.3%; Score 3598; DB 2; Length 888;
 Best Local Similarity 90.8%; Pred. No. 1,3e-167;
 Matches 704; Conservative 9; Mismatches 6; Indels 56; Gaps 2;
 QY 1 MSSARPTPLTNRDPTGLGLDPSKSNMIRGNATSADQPHIGNVRLKTTIG 60
 DB 1 MSSARPTPLTNRDPTGLGLDPSKSNMIRGNATSADQPHIGNVRLKTTIG 60
 QY 61 KGNPAKYLARHLITGGEVAVKIIDKTQLNSSLQKLFREVRIMKUNHNRYKLFVIE 120
 DB 61 KGNPAKYLARHLITGGEVAVKIIDKTQLNSSLQKLFREVRIMKUNHNRYKLFVIE 120
 QY 121 TEKTLVLMRYASGEVFDLVVHGRMKKEAKAPQVAVAYQCHQKFTVHRDLKAEN 180
 DB 121 TEKTLVLMRYASGEVFDLVVHGRMKKEAKAPQVAVAYQCHQKFTVHRDLKAEN 180
 QY 121 TEKTLVLMRYASGEVFDLVVHGRMKKEAKAPQVAVAYQCHQKFTVHRDLKAEN 180
 DB 121 TEKTLVLMRYASGEVFDLVVHGRMKKEAKAPQVAVAYQCHQKFTVHRDLKAEN 180
 QY 181 LLLDADWNKIDAFGEFSNEFTFGNKLDTFCGSPPYAAPLFGCKYDGPEDVWSLGVL 240
 DB 181 LLLDADWNKIDAFGEFSNEFTFGNKLDTFCGSPPYAAPLFGCKYDGPEDVWSLGVL 240
 QY 241 YTVVSGSLPDPGONLKLRRVYRGKRIFFPMSTDCENLKKFLINPESKGTLEIMK 300
 DB 241 YTVVSGSLPDPGONLKLRRVYRGKRIFFPMSTDCENLKKFLINPESKGTLEIMK 300
 QY 301 DRMMVNGHEDELKPYEPLPDYKDPRTPLMTSMGTREIDSLVGQRYNEVMAIYLL 360
 DB 301 DRMMVNGHEDELKPYEPLPDYKDPRTPLMTSMGTREIDSLVGQRYNEVMAIYLL 360
 QY 301 DRMMVNGHEDELKPYEPLPDYKDPRTPLMTSMGTREIDSLVGQRYNEVMAIYLL 360
 DB 301 DRMMVNGHEDELKPYEPLPDYKDPRTPLMTSMGTREIDSLVGQRYNEVMAIYLL 360
 QY 361 LGYKSSLEBDDITTLKPRPSADLTNSAPSPSHKVSANPKNRFSQDAGPALPTSN 420
 DB 361 LGYKSSLEBDDITTLKPRPSADLTNSAPSPSHKVSANPKNRFSQDAGPALPTSN 420
 QY 421 SYKKTQSNNAENKRPEDRESGRKASSTAKVPASPLGLERKKTPTPTSTNSVLSSTN 480
 DB 421 SYKKTQSNNAENKRPEDRESGRKASSTAKVPASPLGLERKKTPTPTSTNSVLSSTN 480
 QY 421 SYKKTQSNNAENKRPEDRESGRKASSTAKVPASPLGLERKKTPTPTSTNSVLSSTN 480
 DB 421 SYKKTQSNNAENKRPEDRESGRKASSTAKVPASPLGLERKKTPTPTSTNSVLSSTN 480
 QY 481 RSNNSPLTERASLGQASISONGKD----- 503
 DB 479 RSNNSPLTERASLGQASISONGKD----- 503
 QY 504 -----STAPQRPVAPSPAHNISSSGAPDRTPRGVSSSTFPAQ 546
 DB 539 KASGLPTTESNCEVPRSTAPQRPVAPSPAHNISSSGAPDRTPRGVSSSTFPAQ 598
 QY 547 LRQVRDQONLPYCVTPASPSGHSQGRGASGIFSKFTSKFVRNINLNPESKQVETLRP 606
 DB 599 LRQVRDQONLPYCVTPASPSGHSQGRGASGIFSKFTSKFVRNINLNPESKQVETLRP 658
 QY 607 HVGSGNDKEKEKEPEBAKRSRFTMSMTTSSMBENEMRRIKVLNDNSCSELEH 666
 DB 659 HVGSGNDKEKEKEPEBAKRSRFTMSMTTSSMBENEMRRIKVLNDNSCSELEH 718
 QY 667 YMLLCHGTPGHEDFYQWEMEVCKLPRLSLNGVRFKRIISGTSNAFQVIAASKIANE 721
 DB 719 YMLLCHGTPGHEDFYQWEMEVCKLPRLSLNGVRFKRIISGTSNAFQVIAASKIANE 773
 RESULT 6
 ID Q96RG0 PRELIMINARY; PRT; 691 AA.
 AC Q96RG0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Ser/Thr protein kinase PAR-1balpha.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2132471; PubMed=11433294; DOI=10.1038/35083016;
RA Sun T.O., Lu B., Feng J.J., Reinhard C., Yan Y.N., Fantl W.J.,
RA Williams L.T.;
RT "PAR-1 is a Dishevelled-associated kinase and a positive regulator of
RT Wnt signalling.";
RL Nat. Cell Biol. 3:628-636(2001).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR HEMBL; AF387638; AAK82368.1; -.
DR HSSP; P24941; 1010.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001772; Kinase_Cterm.
DR InterPro; IPR011009; Kinase_Like.
DR InterPro; IPR002290; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_kinase.
DR InterPro; IPR000449; UBA.
DR InterPro; IPR009060; UBA_Like.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; Kinase; 1.
DR Pfam; PF00627; UBA; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00165; UBA; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50030; UBA; 1.
KM ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 691 AA; 77631 MW; 2216B4AE7BCF31BE CRC64;
Query Match 95.4%; Score 3566; DB 2; Length 691;
Best Local Similarity 99.9%; Pred. No. 3.4e-16;
Matches 690; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
34 MIRGNSATSDADPHIGNYRLKTTIGKGNFAKYKLAARHLLTGKEVAVKIIDKTQUNSSS 93
1 MIRGNSATSDADPHIGNYRLKTTIGKGNFAKYKLAARHLLTGKEVAVKIIDKTQUNSSS 60
94 LQKLFEVRIMKVLNHNIVKLFEVIFETKTLVLMVEYASGGEVFDYLVAGRMKEKEAR 153
61 LQKLFEVRIMKVLNHNIVKLFEVIFETKTLVLMVEYASGGEVFDYLVAGRMKEKEAR 120
154 AKFRQVSAVOYCHQKFIYHRDLKAENLLDADMMIKIADPFGRSNEFTGKDKTCGSP 213
121 AKFRQVSAVOYCHQKFIYHRDLKAENLLDADMMIKIADPFGRSNEFTGKDKTCGSP 180
214 PYAAPBLFQKKYDGEVDVMSLGVLLYTLVSGSLPFDGQNLKELREYLRGKYRIPFYM 273
181 PYAAPBLFQKKYDGEVDVMSLGVLLYTLVSGSLPFDGQNLKELREYLRGKYRIPFYM 240
274 STDCENLLKKEFLINSKSGTLEQIMKDRMNVGHEDEKPYVEBLPYDKPRRTLEAV 333
241 STDCENLLKKEFLINSKSGTLEQIMKDRMNVGHEDEKPYVEBLPYDKPRRTLEAV 300
334 SMGYTREIIODSLVGORVNEVMATYLLLGYSSELEGGDTTLKPRSDADLUNSSAPSPH 393
301 SMGYTREIIODSLVGORVNEVMATYLLLGYSSELEGGDTTLKPRSDADLUNSSAPSPH 360
394 KYQVRSVSNPKQRFSDQAPALPTGNSYSKKTQSNNAENKREEDRESGRKASSTAKVP 453
361 KYQVRSVSNPKQRFSDQAPALPTGNSYSKKTQSNNAENKREEDRESGRKASSTAKVP 420
454 ASPLBLEKKTTPSTSTSVLSTTNRSNPLRLERASIGQASIONGOSTAPQAVPYA 513
421 ASPLBLEKKTTPSTSTSVLSTTNRSNPLRLERASIGQASIONGOSTAPQAVPYA 480

QY 514 SPFAHNISSGGAPDRTNPRGVSSRSTETHAGOLROYRQONLRYGVTPASPSGSGRR 573
DB 481 SPFAHNISSGGAPDRTNPRGVSSRSTETHAGOLROYRQONLRYGVTPASPSGSGRR 540
QY 574 GASGSIFSKFTSKFYVRNINPEPSKDRVETLRLPHVVGSGGNKEKEEFREAKPRSLRFTW 633
DB 541 GASGSIFSKFTSKFYVRNINPEPSKDRVETLRLPHVVGSGGNKEKEEFREAKPRSLRFTW 600
QY 634 SKTTSSMEPNMREIRVLDANSQSELEHKYMLCMHGTGPHEDFVQWMEVCKLPR 693
DB 601 SKTTSSMEPNMREIRVLDANSQSELEHKYMLCMHGTGPHEDFVQWMEVCKLPR 660
QY 694 LSLNGVFRFRISGTSAFNIASKTANIELK 724
DB 661 LSLNGVFRFRISGTSAFNIASKTANIELK 691

RESULT 7

ID Q15524 PRELIMINARY; PRT; 745 AA.
AC Q15524;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
DE Serine/threonine protein kinase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=9839968; PubMed=9730619;
RA Espinosa L., Navarro E.;
RT "Human serine/threonine protein kinase EMK1: genome structure and cDNA
RT cloning of isoforms produced by alternative splicing.";
RL Cytogenet. Cell Genet. 81:278-282(1998).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; X87630; CAA66229.1; -.
DR FIR; G01025; G01025.
DR HSSP; P24941; 1010.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR InterPro; IPR000001; Prot_kinase; 1.
DR InterPro; IPR001772; Kinase_Cterm.
DR InterPro; IPR011009; Kinase_Like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR008271; Ser_Thr_kinase.
DR InterPro; IPR000449; UBA.
DR InterPro; IPR009060; UBA_Like.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; Kinase; 1.
DR Pfam; PF00627; UBA; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00165; UBA; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50030; UBA; 1.
KM ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 745 AA; 83204 MW; C6EA02EBF62B5DF CRC64;

Query Match 94.1%; Score 3515; DB 2; Length 745;
Best Local Similarity 92.3%; Pred. No. 1.1e-163;
Matches 688; Conservative 1; Mismatches 2; Indels 54; Gaps 1;

QY 34 MIRGNSATSDADPHIGNYRLKTTIGKGNFAKYKLAARHLLTGKEVAVKIIDKTQUNSSS 93
DB 1 MIRGNSATSDADPHIGNYRLKTTIGKGNFAKYKLAARHLLTGKEVAVKIIDKTQUNSSS 60
94 LQKLFEVRIMKVLNHNIVKLFEVIFETKTLVLMVEYASGGEVFDYLVAGRMKEKEAR 153

Db 61 LQKLFREVRIMKVLNHNINIKLFEVIEETKTLVLMVEYASGGEVFDVLVAHGKMEKEAR 120
 QY 154 AKRQVSAVOYCHQKFIYHRDLKAENLLLDADNMIIADPGFSNEFTFGNKLDTFCGSP 213
 Db 121 AKRQVSAVOYCHQKFIYHRDLKAENLLLDADNMIIADPGFSNETFGNKLDTFCGSP 180
 QY 214 PYAPBELFOGKKTGDEVDWMSLGVILYTLVSSGLPFDGONLKELRERVLRGKRIIPFM 273
 Db 181 PYAPBELFOGKKTGDEVDWMSLGVILYTLVSSGLPFDGONLKELRERVLRGKRIIPFM 240
 QY 274 STDCENLLKKFLLINPSKRGTLLEQIMKDRMANNVGHEDDELKPYVEPLPDYKDPRTLEMW 333
 Db 241 STDCENLLKKFLLINPSKRGTLLEQIMKDRMANNVGHEDDELKPYVEPLPDYKDPRTLEMW 300
 QY 334 SMGYTREIODSLVGQRVNEVMATYLLLGKSSLEBDITTLKRPESADLTNSAPSPSH 393
 Db 301 SMGYTREIODSLVGQRVNEVMATYLLLGKSSLEBDITTLKRPESADLTNSAPSPSH 360
 QY 394 KVQSVSANPKQRRFSDQAGPAIPTNSYSKKTQSNNAENKRPEDRESGRKASTAKVP 453
 Db 361 KVQSVSANPKQRRFSDQAGPAIPTNSYSKKTQSNNAENKRPEDRESGRKASTAKVP 420
 QY 454 ASPLPGLERKKTTPPTSTNSVLTSTNRSNPLERASLQDASIQNGKD----- 503
 Db 421 ASPLPGLERKKTTPPTSTNSVLTSTNRSNPLERASLQDASIQNGKSLTWPGRAS 480
 QY 504 -----STAPQVPAVPSAHN 519
 Db 481 TASASAAVSARPRQHKMSASVHPNKASGLPTESNCEVPRSTAPQVPAVPSAHN 540
 QY 520 ISSSGAPDRITNPRGVSSRSTFHAQOLROVRDQNLPGVTPASPSPSGHSGRGAAGSI 579
 Db 541 ISSSGAPDRITNPRGVSSRSTFHAQOLROVRDQNLPGVTPASPSPSGHSGRGAAGSI 600
 QY 580 FSKFTSKFVRNINPEPSKQDVEITLRPHVYVSGGNDKXKEEFREAKRSLRFTWSMKTTS 639
 Db 601 FSKFTSKFVRNINPEPSKQDVEITLRPHVYVSGGNDKXKEEFREAKRSLRFTWSMKTTS 660
 QY 640 SMEPNEMMREIRKVLNANSQSELEHEKYMILCMHGTGHDPIVQMEWEVCRLPRLSINGV 699
 Db 661 SMEPNEMMREIRKVLNANSQSELEHEKYMILCMHGTGHDPIVQMEWEVCRLPRLSINGV 720
 QY 700 RPKRISGTSMAFKNIASKIANELKL 724
 Db 721 RPKRISGTSMAFKNIASKIANELKL 745
 RESULT 8
 07KZ17 PRELIMINARY; PRT: 755 AA.
 AC 07KZ17
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DE 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE MAP/microtubule affinity-regulating kinase 2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SOURCE FROM N.A.
 RA Kohnline N., Chen X., Rolfe A., Halleck A., Hines L., Eisenstein S.,
 RA Koundinya M., Raphael J., Moreira D., Kelley T., Labber J., Lin Y.,
 RL Pheasant M., Farmer A.
 CC Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL: BT007342; AAP3606.1; -.
 DR HSP: Q63450.1A06
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:Protein serine/threonine kinase activity; IEA.
 DR GO: GO:0004713; F:Protein-tyrosine kinase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.

DR Interpro: IPR001772; Kinase Cterm.
 DR Interpro: IPR011009; Kinase like.
 DR Interpro: IPR000719; Proc_kinase.
 DR Interpro: IPR002290; Ser_thr_kinase.
 DR Interpro: IPR008271; Ser_thr_pkin_As.
 DR Interpro: IPR001245; Tyr_kinase.
 DR Interpro: IPR000449; UBA.
 DR Interpro: IPR009060; UBA_like.
 DR Pfam: PR02149; KAI.1.
 DR Pfam: PF00629; Kinase.1.
 DR Pfam: PF00627; UBA.1.
 DR ProDom: PD000001; Proc_kinase.1.
 DR SMART: SM00220; S_TKc.1.
 DR SMART: SM00219; TYRc.1.
 DR SMART: SM00165; UBA.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 DR PROSITE: PS50030; UBA.1.
 KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 755 AA; 84332 MW; 493CD86CD3A4C06 CRC64;
 Query Match 93.8%; Score 3504; DB 2; Length 755;
 Best Local Similarity 91.4%; Pred. No. 4e-163;
 Matches 690; Conservative 1; Mismatches 0; Indels 64; Gaps 3;
 QY 34 MIRGNASATSDADQPHIGNYRLIKTIGKNFAVKLARHILITGEVAVKIIDTQNLSSS 93
 Db 1 MIRGNASATSDADQPHIGNYRLIKTIGKNFAVKLARHILITGEVAVKIIDTQNLSSS 60
 QY 94 LQKLFREVRIMKVLNHNINIKLFEVIEETKTLVLMVEYASGGEVFDVLVAHGKMEKEAR 153
 Db 61 LQKLFREVRIMKVLNHNINIKLFEVIEETKTLVLMVEYASGGEVFDVLVAHGKMEKEAR 120
 QY 154 AKRQVSAVOYCHQKFIYHRDLKAENLLLDADNMIIADPGFSNEFTFGNKLDTFCGSP 213
 Db 121 AKRQVSAVOYCHQKFIYHRDLKAENLLLDADNMIIADPGFSNEFTFGNKLDTFCGSP 180
 QY 214 PYAPBELFOGKKTGDEVDWMSLGVILYTLVSSGLPFDGONLKELRERVLRGKRIIPFM 273
 Db 181 PYAPBELFOGKKTGDEVDWMSLGVILYTLVSSGLPFDGONLKELRERVLRGKRIIPFM 240
 QY 274 STDCENLLKKFLLINPSKRGTLLEQIMKDRMANNVGHEDDELKPYVEPLPDYKDPRTLEMW 333
 Db 241 STDCENLLKKFLLINPSKRGTLLEQIMKDRMANNVGHEDDELKPYVEPLPDYKDPRTLEMW 300
 QY 334 SMGYTREIODSLVGQRVNEVMATYLLLGKSSLEBDITTLKRPESADLTNSAPSPSH 393
 Db 301 SMGYTREIODSLVGQRVNEVMATYLLLGKSSLEBDITTLKRPESADLTNSAPSPSH 360
 QY 394 KVQSVSANPKQRRFSDQAGPAIPTNSYSKKTQSNNAENKRPEDRESGRKASTAKVP 452
 Db 361 KVQSVSANPKQRRFSDQAGPAIPTNSYSKKTQSNNAENKRPEDRESGRKASTAKVP 420
 QY 453 PASPLPGLERKKTTPPTSTNSVLTSTNRSNPLERASLQDASIQNGKD----- 503
 Db 421 PASPLPGLERKKTTPPTSTNSVLTSTNRSNPLERASLQDASIQNGKSLTWPGRAS 480
 QY 504 -----STAPQVPAVPSAHN 518
 Db 481 STASASAAVSARPRQHKMSASVHPNKASGLPTESNCEVPRSTAPQVPAVPSAHN 540
 QY 519 NISSSGAPDRITNPRGVSSRSTFHAQOLROVRDQNLPGVTPASPSPSGHSGRGAAGSI 578
 Db 541 NISSSGAPDRITNPRGVSSRSTFHAQOLROVRDQNLPGVTPASPSPSGHSGRGAAGSI 600
 QY 579 IFSKFTSKFV-----RRNLNPEPSKQDVEITLRPHVYVSGGNDKXKEEFREAKRSL 629
 Db 601 IFSKFTSKFVRRNLNPEPSKQDVEITLRPHVYVSGGNDKXKEEFREAKRSL 660
 QY 630 RFTWSMKTTSMEPNEMMREIRKVLNANSQSELEHEKYMILCMHGTGHDPIVQMEWEVC 689
 Db 661 RFTWSMKTTSMEPNEMMREIRKVLNANSQSELEHEKYMILCMHGTGHDPIVQMEWEVC 720

RA Richards S.; Morley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;
 RA Villalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
 RA Pehey J.; Helton E.; Kettman M.; Madan A.; Rodriguez S.; Sanchez A.;
 RA Whitting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;
 RA Blakeley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
 RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.;
 RA Krzyzanski M.I.; Skalska U.; Smallus D.E.; Scherch A.; Schein J.B.;
 RA Jones S.J.; Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22341123; Pubmed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L.; Strausberg R.L.; Wagner L.; Pontius J.; Clifton S.W.;
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT Initiative";
 RL Dev. Dyn. 225:384-391 (2002).
 RL [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S.; Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL: BC043730; AAH43730.1; -.
 DR HSSP: P24941; IOIQ.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:Protein serine/threonine kinase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR001772; Kinase_Cterm.
 DR InterPro: IPR011003; Kinase_Like.
 DR InterPro: IPR000719; Prot_Kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR InterPro: IPR000449; UBA.
 DR Pfam: PF02149; KAI.1.
 DR Pfam: PF00069; Pkinase.1.
 DR ProDom: PD000001; Prot_Kinase.1.
 DR SMART: SM00220; S_TKc.1.
 DR SMART: SM00165; UBA.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 DR PROSITE: PS00106; PROTEIN_KINASE_ST.1.
 DR PROSITE: PS50030; UBA.1.
 DR KMW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 776 AA; 86805 MW; EC7BAD6C6362227 CRC64;
 Query Match 85.5%; Score 3195.5; DB 2; Length 776;
 Best Local Similarity 79.7%; Pred. No. 4,76-148;
 Matches 620; Conservative 56; Mismatches 43; Indels 59; Gaps 6;
 QY 3 SARTPTLNERBTOPTLGHLDSPK-----SSKSNMIRGNS-ATSDQPHIGNYRLK 57
 DB 2 TTTPTLPTVERDADPDALGHADOKTSSSSSKPMILKRTSIAITLADDEPHIGNYRLK 61
 QY 58 TIGKGNPAKYKLARHLITGKEVAVKIIDKTOLNSSSLQKLFREVRIMKVLNHNPIVLF 117
 DB 62 TIGKGNPAKYKLARHLITGKEVAVKIIDKTOLNSSSLQKLFREVRIMKVLNHNPIVLF 121
 QY 118 VITEKTLVIMVEYASGGEVFDYLVAGRMKEKEAKKFGVVSAYOYCHQKTIIVHDLK 177
 DB 122 VITEKTLVIMVEYASGGEVFDYLVAGRMKEKEAKKFGVVSAYOYCHQKTIIVHDLK 181
 QY 178 AENLLDADWNITKIDPFGSNEFTFGNKLDTFCGSPPYAAPLFOGKKYDGPEDVWSLG 237
 DB 182 AENLLDSDMNITKIDPFGSNEFTFGNKLDTFCGSPPYAAPLFOGKKYDGPEDVWSLG 241
 QY 238 VILYTLVSGSLPFDGQNLKELRERVLKGYRIPIFYMSDCEMLKKFLINPSKRGTL 297
 DB 242 VILYTLVSGSLPFDGQNLKELRERVLKGYRIPIFYMSDCEMLKKFLINPSKRGTL 301

QY 298 IMKDRMNVNVEHDEDLKPYVEPLPDYKDPRTTELNVSMGYTRREIODSLVGORYNEVMT 357
 DB 302 IMKDRMNVNVEHDEDLKPYVEPLPDYKDPRTTELNVSMGYTRREIODSLVGORYNEVMT 361
 QY 358 YLLGLYKSSSELLEDITTLKRPASADLTNSAPSPSHKQVSVANPKQKRSFDOAGPAIP 417
 DB 362 YLLGLYKSSSELLEDITTLKRPASADLTNSAPSPSHKQVSVANPKQKRSFDOAGPAIP 421
 QY 418 TSNYSKKTQSNNAENKRRPEDESGRKASSTAKVPASPLPGLEKKTTPPTSTNSVLST 477
 DB 422 NSNSYSKKTQSNNAENKRRPEDESGRKASSTAKVPASPLPGLEKKTTPPTSTNSVLST 481
 QY 478 STNRSNSPLLERASIQASIONGKD----- 503
 DB 482 GTNRSNSPLLERASIQASIONGKD----- 511
 QY 504 -----STAPQVPVAPSPAHNISSGAGADRTNPPRGVSSRTFFAGOL 547
 DB 542 SKPAPSLGNCVDYQRPSTAPQVPVAPSPAHNISSGAGADRTNPPRGVSSRTFFAGOL 599
 QY 548 RQVRDQONLPGY-VTPASPSGHSQGRGASGSIFFSKFTSKFVRNLNBPESKQVETLAP 606
 DB 600 RQVRDQONLPGY-VTPASPSGHSQGRGASGSIFFSKFTSKFVRNLNBPESKQVETLAP 659
 QY 607 HVGSGGNDKEKEKEPEAKRSLRFTWMSKTTSSMBENEMMRRLRYKVLNANSCOSELHEK 666
 DB 660 H-LSVVDKEDKNDHDSKRSRLFTWMSKTTSSMBENEMMRRLRYKVLNANSCOSELHEK 718
 QY 667 YMLLCMHGTGPHEDFYQWEMEVCKLPRLSLNGVRFKRISSGTSNAFKNIANKIELTL 724
 DB 719 YMLLCMHGTGPHEDFYQWEMEVCKLPRLSLNGVRFKRISSGTSNAFKNIANKIELTL 776
 RESULT 11
 Q8QGV3 PRELIMINARY; PRT; 785 AA.
 ID 08QGV3;
 AC 08QGV3;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Serine/threonine kinase.
 GN Name=MARK2;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Oocyte;
 RA Nakajo N.; Shimuta K.; Uto K.; Sagata N.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL: AB071963; BAB86594.1; -.
 DR HSSP: P24941; IOIQ.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:Protein serine/threonine kinase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR001772; Kinase_Cterm.
 DR InterPro: IPR011003; Kinase_Like.
 DR InterPro: IPR000719; Prot_Kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR InterPro: IPR000449; UBA.
 DR Pfam: PF02149; KAI.1.
 DR ProDom: PD000001; Prot_Kinase.1.
 DR SMART: SM00069; Pkinase.1.
 DR SMART: SM00220; S_TKc.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.

QY 487 LLEBASLGQASIONGKD----- 503
: : : : :
DB 497 MLDRATLVPSGSIHNGKDSFMSPGSRASTASAPATSARIHQKSMSTSVHPKRAPSLDG 556
QY 504 -----STAPORVPVAPSAHNISSSGGAAPDRTNPRGVSSNSTFHAGOLROYDQONT 556
: : : : :
DB 557 NCDVQRASSTAPORLPVSSPSAHNISSA--ATERNNPRGVSSNSTFHAGVQRARDQONTL 614
QY 557 PYGTPAPSPGSGHGRGASGSI FSKFTSKFVRNRLNEPESKDRVETLRPHVVGSGNDK 616
: : : : :
DB 615 GF-VSPSPSGISQGRGATGSI FSKFTSKFVRKNPDPEKORVESTTRPH-LSVDKKEK 672
QY 617 EKEEPREAKPRSLRFTWSMKTSSMEPNEMREIRKYLNDANSQSELEHEKMLCMHGTPT 676
: : : : :
DB 673 DKEDLNDKSRSLRFTWSMKTSSMEPNEMSEICKLDANNCOYESODKTMLLCVHGTPT 732
QY 677 GHEDPVQWEMEVCKLPRLSLNGVRFKRI SGTSMAPKNIASKIANELKL 724
733 GHNDVQWEMEVCKLPRLSLNGVRFKRI SGTSMAPKNIASKIANDELKL 780
DB
RESULT 13
QYVHUS PRELIMINARY; PRT; 795 AA.
AC QYVHUS;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Eukl motif serine-threonine protein kinase 3.
GN Name=Mark1; Synonym=Emk3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Darnon Y.M., Le Morvan V.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AF453686; AAL50826.1; -.
DR HSSP; P24941; 10IO.
DR MGD; MGI:2664902; Mark1.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; PKinase; 1.
DR Pfam; PF00627; UBA; 1.
DR ProDom; PD000001; Proc_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00165; UBA; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00300; UBA; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 795 AA; 88545 MW; 79A74E2EE9A35A2 CRC64;
Query Match 68.5%; Score 2561; DB 2; Length 795;
Boot local similarity 65.6%; Pred. No. 4.6e-117;
Matches 528; Conservative 81; Mismatches 102; Indels 94; Gaps 15;
QY 3 SARTPLPTLNERDTEOPTL--GHLD-----SKPSSKSNMIRGNNSATSA--DEOPHIGNVR 54
: : : : :
DB 2 SARTPLPTVNERDTEHNTSVDTYTERFIPTTKSSSRQNIIRCHNSITSATDEQPHIGNVR 61
QY 55 LKLTIGKGNPAKYLARHILITGKEVAVKIIDKQOLNSSSLQKIFREIRIKVLNHPRIYK 114
: : : : :
DB 62 LQKTIIGNGNPAKYLARHVLITGRBVAVKIIDKQOLNPTSLQKIFREIRIKVLNHPRIYK 121
QY 115 LPEVIEETKTLVLMVEYASGEVFDVLVAHGKKEKARAKFRQVAVQYCHQKFIYHR 174

DB 122 LPEVIEETKTLVLMVEYASGEVFDVLVAHGKKEKARAKFRQIVASVQYCHQKFIYHR 181
QY 175 DLKAENILLADAMNIIKIDFGFSENEFTFGKLDLTFPGSPYYAABELFQKKYDPEVDVW 234
DB 182 DLKAENILLADAMNIIKIDFGFSENEFTFGKLDLTFPGSPYYAABELFQKKYDPEVDVW 241
QY 235 SLGVIIYTLVSGSLPDPGQNLKELRKYLRGKTRIPYMSYTDENLLKKPLINPSRGT 294
: : : : :
DB 242 SLGVIIYTLVSGSLPDPGQNLKELRKYLRGKTRIPYMSYTDENLLKKPLINPIRGS 301
QY 295 LEQIMKDRMNVNHEDELPYVEPLPDYKDPRTTELIMVSMGYTREIOPSLVQORYNEV 354
DB 302 LEQIMKDRMNVNHEDELPYVEPLPDYKDPRTTELIMVSMGYTREIOPSLVQORYNEV 361
QY 355 MATYLLIGYKSSLEGG-----DTTLKPPPSADLTNSAPSPSH-KVQSVANPKQR 407
: : : : :
DB 362 MATYLLIGYKSSLEGG-----DTTLKPPPSADLTNSAPSPSH-KVQSVANPKQR 421
QY 408 FSDQAGPAIPITNSYSKQTQSNNAENKRPPE--DREGSKASST-----AKVPASPPLGLE 461
: : : : :
DB 422 FSDHAGPSLPPAVSYTRPQANSVESEKQEWKDTARRLSITVGSKESEVTASPLVGP 481
QY 462 RKKTPTPTSTNSVLTSTNRSRNSPLLERASLGQASIONGKST----- 505
: : : : :
DB 482 RKGSTASPS-NVYSGSGMAKRTTYCERSTDRYALQNGRDSLTMSGASSMSGSTV 540
: : : : :
QY 506 -----APQRPVAPSAHNISSSGA 526
DB 541 ASAGPAPRPHQKSMSTSGHPIKVTLPTIKDGEAVRPGAQIVPAAPSAHISAS--T 598
QY 527 PDRTPNPRGVSSSTHAGOLROYDQONTLPYGTASPSGSGG-----RRGASGIF 581
: : : : :
DB 599 PDRTPNPRGVSSSTHAGOLROYDQONTLPYGTASPSGSGG-----RRGASGIF 654
QY 582 KFTSKFVRNRLNEPESKDRVETLRPHVVGSGNDKE--KEEPREAKPRSLRFTWSMKTSS 639
: : : : :
DB 655 KITSKVRNDRPSRGEASGRDTRAR-----GSSGPKRDEEGEAKPRSLRFTWSMKTSS 710
QY 640 SMEPNEMREIRKYLNDANSQSELEHEKMLCMHGTPTGHEDPVQWEMEVCKLPRLSLNGV 699
DB 711 SMDPNMLREIRKYLNDANTCDYEQKERFLLFCVHGDAQQSIVQWEMEVCKLPRLSLNGV 770
QY 700 RFRISIGTSMAPKNIASKIANELKL 724
DB 771 RFRISIGTSMAPKNIASKIANDELKL 780
RESULT 14
ID 008678 PRELIMINARY; PRT; 793 AA.
AC 008678;
DT 01-JUL-1997 (T-EMBLrel. 04, Created)
DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Serine/threonine kinase.
GN Name=mark1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RA MEDLINE=97262070; Pubmed=9108484; DOI=10.1016/S0092-8674(00)80208-1;
RA Drewes G., Ebnech A., Preuss U., Mandelkow E., Mandelkow E.;
RT "MARK - a Novel Family of Protein Kinases that Phosphorylate
Microtubule-associated Proteins and Trigger Microtubule Disruption.";
Cell 89:297-308(1997).
RL EMBL; Z63868; CAB06294.1; -.
DR HSSP; P24941; 10IO.
DR GO; GO:0005524; F:ATP binding; IEA.

DR GO: GO:004674; F:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR011772; Kinase_Cterm.
 DR InterPro: IPR011009; Kinase_Like.
 DR InterPro: IPR000719; Prot_Kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR InterPro: IPR000449; UBA.
 DR Pfam: PF02149; KAI; 1.
 DR Pfam: PF00069; PKinase; 1.
 DR Pfam: PF00627; UBA; 1.
 DR Prodom: PD000001; Prot_Kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00165; UBA; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS00030; UBA; 1.
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 KM ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 793 AA; 88234 MW; C5BCAC0BB9A0A3 CRC64;

Query Match 68.4%; Score 2555; DB 2; Length 793;

Best Local Similarity 65.5%; Pred. No. 9e-117;
 Matches 525; Conservative 82; Mismatches 105; Indels 90; Gaps 14;

3 SARTPLPTLNERTDEPTL--GHLD-----SKPSSKSNMIRGNATS-DEOPHIGNR 54
 2 SARTPLPTVNERTDENTSVDTGETHIPTKSSSRQNI PRCHNSITSATDEQPHIGNR 61
 55 LKTTGKGNPAKYLAHHITGKEVAVKIIDKTQUNSSLOKLFREVRIMKVLNHPNIYK 114
 62 LKTTGKGNPAKYLAHHITGKEVAVKIIDKTQUNSSLOKLFREVRIMKVLNHPNIYK 121
 115 LFEVTEKTLTYLMEYASGGEVFDYLAHGRMKEKARAFKQVAVOYCHQKFIYHR 174
 122 LFEVTEKTLTYLMEYASGGEVFDYLAHGRMKEKARAFKQVAVOYCHQKFIYHR 181
 175 DLKAEMLLDADNMNIKIADFGFNEFTFGNKLDTFGSPYPAABELFOGKKYDGEVDW 234
 182 DLKAEMLLDADNMNIKIADFGFNEFTFGNKLDTFGSPYPAABELFOGKKYDGEVDW 241
 235 SLGVTITLVSGSTPRPGONKELREVLGKRIIPYMSDGCNLLKFKFIINPSKRG 294
 242 SLGVTITLVSGSTPRPGONKELREVLGKRIIPYMSDGCNLLKFKFIINPSKRG 301
 295 LEQIMKRMWNVGHEDELKPYEPLDPDYKDPRTTELMVSGYTRIEI QDSLVGQRYNEV 354
 302 LEQIMKRMWNVGHEDELKPYEPLDPDYKDPRTTELMVSGYTRIEI QDSLVGQRYNEV 361
 355 MATYLLIGYKSSLELG-----DITTLKPRPSALUTNSSAPSPH-KYQPSVSNPRQR 407
 362 MATYLLIGYKSSLELG-----DITTLKPRPSALUTNSSAPSPH-KYQPSVSNPRQR 421
 408 FSDGAPAIPTNSYSKKTQSNNAENKRPPE-DRESGKRAST-----AKVPASPLGLE 461
 422 FSDHAGPEIIPAVSYTKRPQANSVSEBQKEWMDKDTARLGSTTVGSGSEVTAAPLVGP 481
 462 RKTTPTPSTNSVLSTSTNRNSPLERASLQASIONKDS----- 504
 482 RKSSAGPS-NNVVSGSGMTRNTYVCERSTDRYALQNGRDSLITEMSASMSGTSIV 540
 505 -----TAP-----ORVPVASPSAHNISSSGA 526
 541 ASAGSAPRPHQKSNSTSGHPIKVTLLPTIKGSEAYRPGTAKRVPASPSAHNISAS--T 598
 547 PDRTNFPRGVSSSTFHAQQLQVADQONLPGYVTPASPS-----GHSQGRGASGSIIFS 582
 559 PDRTFPRGSSSRSTFHGEQL--RRRSAAVSGPPASPSHDYALAHARAGTSTGISTSK 655
 583 FTSKFRNLNPESSKDRVETLRPHVVGSGNDKKEFRKAPKPSLAFVTSMTKTSME 642
 656 ITSKEVRBDPSEGEASGRITDAR-----GSSGEPKDEGKKEKAPRSISLFTVSMKTTSMD 711

QY 643 PNEMRIRIKYLDANSCQSEIHEKYMLLCMHGTPGHEDFYQWMEVCKLPRLSLNGVRFK 702
 DB 712 PNDWVREIRKYLNDNTDYQREKRFLLFCVHGARDQDSLVOYMEVCKLPRLSLNGVRFK 771
 QY 703 RISGTSMAFKNIASKIANELKL 724
 DB 772 RISGTSIAFKNIASKIANELKL 793

RESULT 15

QY 643 PNEMRIRIKYLDANSCQSEIHEKYMLLCMHGTPGHEDFYQWMEVCKLPRLSLNGVRFK 702

DB 712 PNDWVREIRKYLNDNTDYQREKRFLLFCVHGARDQDSLVOYMEVCKLPRLSLNGVRFK 771

QY 703 RISGTSMAFKNIASKIANELKL 724

DB 772 RISGTSIAFKNIASKIANELKL 793

QY 643 PNEMRIRIKYLDANSCQSEIHEKYMLLCMHGTPGHEDFYQWMEVCKLPRLSLNGVRFK 702

DB 712 PNDWVREIRKYLNDNTDYQREKRFLLFCVHGARDQDSLVOYMEVCKLPRLSLNGVRFK 771

QY 703 RISGTSMAFKNIASKIANELKL 724

DB 772 RISGTSIAFKNIASKIANELKL 793

QY 643 PNEMRIRIKYLDANSCQSEIHEKYMLLCMHGTPGHEDFYQWMEVCKLPRLSLNGVRFK 702

DB 712 PNDWVREIRKYLNDNTDYQREKRFLLFCVHGARDQDSLVOYMEVCKLPRLSLNGVRFK 771

QY 703 RISGTSMAFKNIASKIANELKL 724

DB 772 RISGTSIAFKNIASKIANELKL 793

QY 643 PNEMRIRIKYLDANSCQSEIHEKYMLLCMHGTPGHEDFYQWMEVCKLPRLSLNGVRFK 702

DB 712 PNDWVREIRKYLNDNTDYQREKRFLLFCVHGARDQDSLVOYMEVCKLPRLSLNGVRFK 771

QY 703 RISGTSMAFKNIASKIANELKL 724

DB 772 RISGTSIAFKNIASKIANELKL 793

QY 643 PNEMRIRIKYLDANSCQSEIHEKYMLLCMHGTPGHEDFYQWMEVCKLPRLSLNGVRFK 702

DB 712 PNDWVREIRKYLNDNTDYQREKRFLLFCVHGARDQDSLVOYMEVCKLPRLSLNGVRFK 771

QY 703 RISGTSMAFKNIASKIANELKL 724

DB 772 RISGTSIAFKNIASKIANELKL 793

QY 643 PNEMRIRIKYLDANSCQSEIHEKYMLLCMHGTPGHEDFYQWMEVCKLPRLSLNGVRFK 702

DB 712 PNDWVREIRKYLNDNTDYQREKRFLLFCVHGARDQDSLVOYMEVCKLPRLSLNGVRFK 771

QY 703 RISGTSMAFKNIASKIANELKL 724

DB 772 RISGTSIAFKNIASKIANELKL 793

QY 643 PNEMRIRIKYLDANSCQSEIHEKYMLLCMHGTPGHEDFYQWMEVCKLPRLSLNGVRFK 702

DB 712 PNDWVREIRKYLNDNTDYQREKRFLLFCVHGARDQDSLVOYMEVCKLPRLSLNGVRFK 771

QY 703 RISGTSMAFKNIASKIANELKL 724

DB 772 RISGTSIAFKNIASKIANELKL 793

QY 643 PNEMRIRIKYLDANSCQSEIHEKYMLLCMHGTPGHEDFYQWMEVCKLPRLSLNGVRFK 702

DB 712 PNDWVREIRKYLNDNTDYQREKRFLLFCVHGARDQDSLVOYMEVCKLPRLSLNGVRFK 771

QY 703 RISGTSMAFKNIASKIANELKL 724

DB 772 RISGTSIAFKNIASKIANELKL 793

QY 643 PNEMRIRIKYLDANSCQSEIHEKYMLLCMHGTPGHEDFYQWMEVCKLPRLSLNGVRFK 702

DB 712 PNDWVREIRKYLNDNTDYQREKRFLLFCVHGARDQDSLVOYMEVCKLPRLSLNGVRFK 771

QY 703 RISGTSMAFKNIASKIANELKL 724

DB 772 RISGTSIAFKNIASKIANELKL 793

QY 643 PNEMRIRIKYLDANSCQSEIHEKYMLLCMHGTPGHEDFYQWMEVCKLPRLSLNGVRFK 702

DB 712 PNDWVREIRKYLNDNTDYQREKRFLLFCVHGARDQDSLVOYMEVCKLPRLSLNGVRFK 771

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